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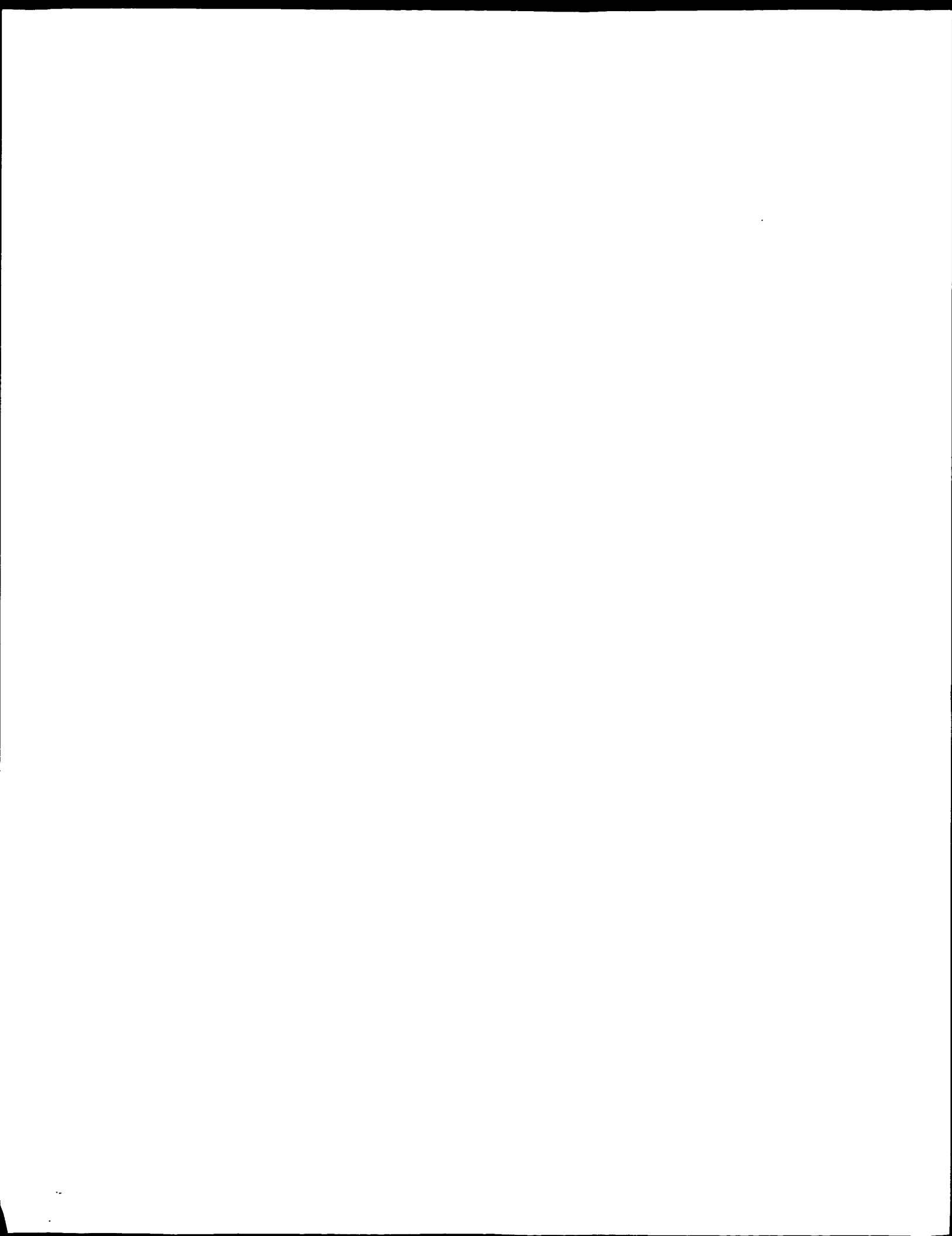
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_____ APS
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_____ SDC
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_____ Other CGN



DR N-PSDB; ABL92103.
 XX
 PT An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 XX marker (TEM) protein, useful for inhibiting tumor growth -
 PS Claim 1; Page 206-207; 331pp; English.
 XX
 CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neovascularisation in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
 XX
 SQ Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 23; Length 500;
 Best Local Similarity 100.0%; Pred. No. 1.4e-250;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELMLLVLLVREARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEFDR 60
 DB 1 MRGELMLLVLLVREARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEFDR 60
 QY 61 TQSLDGLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELRVWDAEANSRQVK 120
 DB 61 TQSLDGLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELRVWDAEANSRQVK 120
 QY 121 IHTILSNTHRQASRVVLSFDFPFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180
 DB 121 IHTILSNTHRQASRVVLSFDFPFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180
 QY 181 NFNPGYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
 DB 181 NFNPGYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
 QY 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDFSKVTSMAVEFTP 300
 DB 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDFSKVTSMAVEFTP 300
 QY 301 LPTCLQHRSCDACMSDITFNCSCWCHVLQRCSSGFORYRQEWMDYGCQAQEAEGRMCEDFQ 360
 DB 301 LPTCLQHRSCDACMSDITFNCSCWCHVLQRCSSGFORYRQEWMDYGCQAQEAEGRMCEDFQ 360
 QY 361 DEHDASAPDTSFSPYDGLTTTSSSLFIDSLTETDTKLNPYAGDGLQNNLSPKTKGT 420
 DB 361 DEHDASAPDTSFSPYDGLTTTSSSLFIDSLTETDTKLNPYAGDGLQNNLSPKTKGT 420
 QY 421 PVHLGTGVIGVAVLLVAAILLAGIYNGHTSNAALFIERPHHPWPAKFRSHPDHST 480
 DB 421 PVHLGTGVIGVAVLLVAAILLAGIYNGHTSNAALFIERPHHPWPAKFRSHPDHST 480
 QY 481 YAEVPEPSGHEKEGFMQAEC 500
 DB 481 YAEVPEPSGHEKEGFMQAEC 500

RESULT 2
 ID ABB90723
 XX ABB90723 standard; Protein; 1002 AA.
 AC ABB90723;
 XX
 DT 30-MAY-2002 (first entry)
 XX

DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.
 XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neovascularisation; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.
 XX Homo sapiens.
 OS WO200210217-A2.
 PN 07-FEB-2002.
 PD 01-AUG-2001; 2001WO-US24031.
 PF 02-AUG-2000; 2000US-222599P.
 PR 11-AUG-2000; 2000US-224360P.
 PR 11-APR-2001; 2001US-282850P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA St Croix B, Kinzler KW, Vogelstein B;
 PI WPI; 2002-291856/33.
 DR An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -
 XX Disclosure; Page 125-128; 331pp; English.
 PS The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neovascularisation in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
 XX
 SQ Sequence 1002 AA;

Query Match 100.0%; Score 2691; DB 23; Length 1002;
 Best Local Similarity 100.0%; Pred. No. 4e-250;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELMLLVLLVREARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEFDR 60
 DB 503 MRGELMLLVLLVREARALSPQAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEFDR 562
 QY 61 TQSLDGLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELRVWDAEANSRQVK 120
 DB 563 TQSLDGLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELRVWDAEANSRQVK 622
 QY 121 IHTILSNTHRQASRVVLSFDFPFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 180
 DB 623 IHTILSNTHRQASRVVLSFDFPFYGHPLRQITATGGFIFMGDVIHRLMTATQYVAPLMA 682
 QY 181 NFNPGYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
 DB 683 NFNPGYSDNSTVYVFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 742
 QY 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDFSKVTSMAVEFTP 300
 DB 743 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEYHRIELDFSKVTSMAVEFTP 802
 QY 301 LPTCLQHRSCDACMSDITFNCSCWCHVLQRCSSGFORYRQEWMDYGCQAQEAEGRMCEDFQ 360

Db 803 LPTCLQHRSCDACWSSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 862
 Qy 361 DEDHDSASPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
 Db 863 DEDHDSASPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 922
 Qy 421 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
 Db 923 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 982
 Qy 481 YAEVPSGHEKEGFEAEQC 500
 Db 983 YAEVPSGHEKEGFEAEQC 1002
 RESULT 3
 ABB90729
 ID ABB90729 standard; Protein: 500 AA.
 AC ABB90729;
 XX
 DT 30-MAY-2002 (first entry)
 DE Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.
 XX
 KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.
 XX
 OS Mus musculus.
 XX
 PN WO200210217-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 01-AUG-2001; 2001WO-US24031.
 XX
 PR 02-AUG-2000; 2000US-222599P.
 PR 11-AUG-2000; 2000US-224360P.
 PR 11-APR-2001; 2001US-282850P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI St Croix B, Kinzler KW, Vogelstein B;
 XX
 DR WPI; 2002-291856/33.
 XX
 PT An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -
 XX
 PS Disclosure; Page 146-147; 331pp; English.
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 CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
 XX
 SQ Sequence 500 AA;

Query Match 82.1%; Score 2209; DB 23; Length 500;

Best Local Similarity 81.6%; Pred. No. 4.6e-204;
 Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;
 Qy 1 MRGELWLL-VLVLREARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 59
 Db 1 MRAQLWLLQLLLRGAARALSPATPAGHNEGQDSAWTAKRTQGSRRRPRESPAQLKPG 60
 Qy 60 RTOLSDILGGGTGLAMDTLPDNRTRVVEDNHSYVSLYGPSPHRSRELWVDVAENRSHV 119
 Db 61 KTQLSODLGGGSGLAIDTLPDNRTRVVEDNHNHYVSVYGGKQSDLLWDLAVANRSHV 120
 Qy 120 KIHTILSNTHQASRVVLSFDFPFYGHPLRQITITATGGFIFMGDVIHRLMTATQYVAPLM 179
 Db 121 KIHRILLSSSHRQASRVVLSFDFPFYGHPLRQITITATGGFIFMGDMLHRLMTATQYVAPLM 180
 Qy 180 ANENPGYSDNSTVYFDNGTIVVQNDHVVYLGQWEDKGSFTFOAALHHDGRIVEAYKEIP 239
 Db 181 ANENPGYSDNSTVAYFDNGTIVVQNDHVVYLGQREDRGSFTFOAALHHDGRIVEAYKEIP 240
 Qy 240 MSYPEISSSOHPVKITGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTSMASVEFT 299
 Db 241 MAVLDISSAQHPVKAGLSDAFMINSSPEVPSQRTIFEYHVELDLSKIITTSVAVET 300
 Qy 300 PLPTCLQHRSCDACMSDLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDF 359
 Db 301 PLPTCLQHQSCDTCVSNLTFNCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDF 360
 Qy 360 QDEHDSASPDTSFSPYDGLTFTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKG 419
 Db 361 QDHSYASPDSSFSFPGND- STTSSSLFIDSLTTEDDTKLNYPAGDGLDHSSPKSKG 419
 Qy 420 TPVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHS 479
 Db 420 PPVHLGTIVGIVLAVLLVAAIILAGIYISGHPNSNAALFFIERRPHHPAMKFRSHPDHS 479
 Qy 480 TYAEVPSGHEKEGFEAEQC 500
 Db 480 TYTEVPSGHEKEGFEAEQC 500
 RESULT 4
 ABB90783
 ID ABB90783 standard; Protein: 500 AA.
 XX
 AC ABB90783;
 XX
 DT 30-MAY-2002 (first entry)
 DE Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 297.
 XX
 KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.
 XX
 OS Mus musculus.
 XX
 PN WO200210217-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 01-AUG-2001; 2001WO-US24031.
 PR 02-AUG-2000; 2000US-222599P.
 PR 11-AUG-2000; 2000US-224360P.
 PR 11-APR-2001; 2001US-282850P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI St Croix B, Kinzler KW, Vogelstein B;
 XX
 DR WPI; 2002-291856/33.

DR	N-PSDB; ABL92136.
XX	
PT	An isolated molecule comprising an antibody variable region which
PT	specifically binds to an extracellular domain of a tumor endothelial
PT	marker (TEM) protein, useful for inhibiting tumor growth -
XX	
PS	Disclosure; Page 301-302; 331pp; English.
XX	
CC	The invention relates to an isolated molecule comprising an antibody
CC	variable region which specifically binds to an extracellular domain of a
CC	tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC	ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC	proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC	They are useful for inhibiting tumour growth, neoangiogenesis in
CC	subjects bearing a vascularised tumour, polycystic kidney disease,
CC	diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
CC	and rat TEM genes and the encoded proteins (ABL92073-ABL92141 and
CC	ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
CC	sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
CC	ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
CC	and pan-endothelial markers (PEM) ABL91903-ABL91995.
XX	
SQ	Sequence 500 AA:

DE	Tumour endothelial marker 7 precursor protein.
KW	Stem cell growth factor-like polypeptide; leukemia; hemophilia; human;
KW	degenerative disease; Alzheimer's disease; nutritional supplement;
KW	Cytostatic; neurotropic; neuroprotective; hemostatic; antineoplastic;
KW	gene-therapy; tumour endothelial marker 7 precursor protein.
XX	
OS	Homo sapiens.
XX	
PN	WO200153500-A1.
XX	
PD	26-JUL-2001.
XX	
PF	23-DEC-2000; 2000MO-US35260.
XX	
PR	21-JAN-2000; 2000US-0488725.
PR	07-APR-2000; 2000US-0545714.
PR	11-APR-2000; 2000US-0547358.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Labat I, Tang YT, Drmanac RT, Liu C, Lee J, Mize NK, Childs J;
PI	Chao C;
XX	
DR	WPI: 2001-451909/48.
XX	
PT	Isolated polypeptide with stem cell growth factor-like activity for
PT	treatment of leukemia, hemophilia, and degenerative diseases like
PT	Alzheimer's disease and to generate new tissues and organs -
XX	
PS	Example 4; Page 149-150; 154pp; English.
XX	
CC	The invention provides novel human stem cell growth factor-like
CC	polypeptides and polynucleotides encoding them. The polypeptides having
CC	stem cell growth factor-like activity, can be expressed by standard
CC	recombinant methodology. The polynucleotides and polypeptides can be
CC	used to induce differentiation of embryonic and adult stem cells to give
CC	rise to different cell types. They may also be used in the treatment of
CC	leukemia, hemophilia, and degenerative diseases like Alzheimer's disease.
CC	They may also be utilized to generate new tissues and organs that may be
CC	patients in need of transplants. They can also be used as nutritional
CC	supplements. The present sequence represents a tumour endothelial marke
CC	7 precursor protein, homologous to a stem cell growth factor-like
CC	polypeptide.
XX	
SQ	Sequence 431 AA;
	Query Match 81.2%; Score 2185; DB 22; Length 431;
	Best Local Similarity 95.2%; Pred. No. 7.5e-202;
	Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps
QY	72 LAMDTLPDNRTRVEDNHSYYVSRLYGSPHRSRELVDAEARNRQVKIHTILSNTHRQ 131
Db	1 LAMDTLPDNRTRVEDNHSYYVSRLYGSPHRSRELVDAEARNRQVKIHTILSNTHRQ 60
QY	132 ASRVVLSDFFPYGHPLRQITATGGTFMGCDVIHRMLTATQTVAPLMANFNPGISDNST 191
Db	61 ASRVVLSDFFPYGHPLRQITATGGTFMGCDVIHRMLTATQTVAPLMANFNPGISDNST 120
QY	192 VYFDNGTVFVVQWDHVYLQGWKDGFTFOAALHDGRIVFAFKPIMSVPEISSOHP 251
Db	121 VYFDNGTVFVVQWDHVYLQGWKDGFTFOAALHDGRIVFAFKPIMSVPEISSOHP 180
QY	252 VKTGLSADPMILNPDPVPESRRRSIEFYHRIELDPKVTSMASVEFTPLPTCLOHRSCD 311
Db	181 VKTGLSADPMILNPDPVPESRRRSIEFYHRIELDPKVTSMASVEFTPLPTCLOHRSCD 240
QY	312 ACMSSDLTFNCWSCHVLQRCSGDFRYRQEW-MDYGCQAQEAEGRMCEDFQD-----ED 363
Db	241 ACMSSDLTFNCWSCHVLQRCSGDFRYRQEWDMTCQAQEAEG-----QDVRLGLPGWR 294
QY	364 HDASPDTSFSYPGDGLTTTSSLIIFDSLTETDDTKLNPYAGDGLQNLLSPKTKGTVPV 423

CC	nucleic acids can be used to express ORFX proteins in gene therapy
CC	vectors. the proteins and nucleic acids may be used to treat cancers,
CC	proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC	graft vs host disease, cardiovascular disease, diabetes mellitus, lupus
CC	hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC	erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC	bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC	allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC	nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC	coagulation; to inhibit thrombosis; and as a contraceptive.
XX	
XX	Sequence 400 AA;
XX	Query Match 74.6%; Score 2007; DB 21; Length 400;
XX	Best Local Similarity 100.0%; Pred. No. 1e-184;
XX	Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	1 MRGELMLLVLRRAARALSPQAGHDEGPGSGWAAKGVIRGNRRARESPGHVSEPD 60
Db	29 MRGELMLLVLRRAARALSPQAGHDEGPGSGWAAKGVIRGNRRARESPGHVSEPD 88
Qy	61 TQLSQDLGGTGLAMDTLPNRTRVVYEDNHNHVVYVRLYGPSPHRELWVDVAEANRSQVK 120
Db	89 TQLSQDLGGTGLAMDTLPNRTRVVYEDNHNHVVYVRLYGPSPHRELWVDVAEANRSQVK 148
Qy	121 IHTILSNTHRQASRVVLSDFPFYGHPLRQITATGGPIFMGDVIHRMLTATQYVAPLMA 180
Db	149 IHTILSNTHRQASRVVLSDFPFYGHPLRQITATGGPIFMGDVIHRMLTATQYVAPLMA 208
Qy	181 NFNPGYSDNSTVYVFQNGTVFVQNDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db	209 NFNPGYSDNSTVYVFQNGTVFVQNDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 268
Qy	241 SVPEISSQHPPVKTGLSDAFMLINPSPDVPSPRRRSIFEYHRIELDPKVTSMASVEFTP 300
Db	269 SVPEISSQHPPVKTGLSDAFMLINPSPDVPSPRRRSIFEYHRIELDPKVTSMASVEFTP 328
Qy	301 LPTCLQHRSCDACMSSDLTFNCNCHVLQRCSSGDFRYRQEMWMDYGCQAQEAEGRMCEDFQ 360
Db	329 LPTCLQHRSCDACMSSDLTFNCNCHVLQRCSSGDFRYRQEMWMDYGCQAQEAEGRMCEDFQ 388
Qy	361 DEDHDSASPT 371
Db	389 DEDHDSASPT 399
RESULT 7	
AA85396	
ID	AA85396 standard; Protein; 499 AA.
XX	
AC	AA85396;
XX	
DT	17-SEP-2001 (first entry)
XX	Stem cell growth factor-like polypeptide mature protein.
DE	
XX	Stem cell growth factor-like polypeptide; leukemia; hemophilia; human;
KW	degenerative disease; Alzheimer's disease; nutritional supplement;
KW	cytostatic; nontropic; neuroprotective; hemostatic; antisense-therapy;
KW	gene-therapy; cell proliferation; stem cell growth factor.
XX	
OS	Homo sapiens.
XX	
PN	WO200153500-A1.
XX	
PD	26-JUL-2001.
XX	
PF	23-DEC-2000; 2000WO-US35260.
XX	
PR	21-JAN-2000; 2000US-0488725.
PR	07-APR-2000; 2000US-0545714.
PR	11-APR-2000; 2000US-0547358.
XX	

Db 275 PVKVGSLDAFVVHRIQIPNVRRTIYEHVRLQMSKITNISAVEMTPTLCLOFNRC 334
QY 311 DACMSSDLTFNCWCHVLRQCSGFDYRQWMDYGCQAEGRCMCEDFQDDHDSASPD 370
Db 335 GPCVSSQIGFNCWCKLQRCSSGFDHRRQDWDVSGCPESKEKMCENTPEVETSSRTT 394
QY 371 T--SFSPYDGLTTTS---SSLFIDSLTDEDTKLNYPAGGGLQ--NNLSPKTKGTPVHL 424
Db 395 TIGATTQFRVLTTTRRAVTSQFPTSLPTEDDTKIALHLKNGASTDDSAEKKGTLHA 454
QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPWPKMFKRSHPDHSTYAEV 484
Db 455 GLVIGLILVIVATALLVTVYMHHTPSAASIFFIERRPSRWPKMFKRSGHPAYAEV 514
QY 485 EPSGHEKEGFMEEQC 500
Db 515 EPVG-EKEGFIVSEQ 529

RESULT 9
ABB90726
ID ABB90726 standard; Protein: 529 AA.
XX AC ABB90726;
XX DT 30-MAY-2002 (first entry)
XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 189.
XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis.
XX OS Homo sapiens.
XX PN WO200210217-A2.
XX PD 07-FEB-2002.
XX PF 01-AUG-2001; 2001WO-US24031.
XX PR 02-AUG-2000; 2000US-222599P.
XX PR 11-AUG-2000; 2000US-224360P.
XX PR 11-APR-2001; 2001US-282850P.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2002-291856/33.
XX DR An isolated molecule comprising an antibody variable region which
specifically binds to an extracellular domain of a tumor endothelial
marker (TEM) protein, useful for inhibiting tumor growth -
PS Disclosure; Page 140-141; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
variable region which specifically binds to an extracellular domain of a
tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumor growth, neoangiogenesis in
XX subjects bearing a vascularised tumour, polycystic kidney disease,
XX diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
XX and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
XX ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
XX sequences; tumour endothelial markers (TEM) ABL91996-ABL92041 and
XX ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
XX and pan-endothelial markers (PEM) ABL91903-ABL91995.

Seq Sequence 529 AA;
Query Match 48.1%; Score 1295; DB 23; Length 529;
Best Local Similarity 57.3%; Pred. NO. 8.2e-116;
Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;
QY 72 LAMDTLPNRRVRVED-NHXYVSVRLXGCPSEPHSRLEWVDVAEANRQVQKIHTLSNTHR 130
Db 95 LLLDDGQDNNTQIEEDTDHNYIISRIYGPSDSASRDLWVNDQMEKDKVKIHGLSNTHR 154
QY 131 QASRVVLSFDPFFGHPHQRIQTIATGFIEMGDVHRLMTATQIVAPLMAFNFGYSDNS 190
Db 155 QAARVNLSEDFPFYGHFLREITVATGGFIYTGVEVHRLMTATQIVAPLMAFNDFSVSRNS 214
QY 191 TVVYFDNGTVFVQMDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 215 TVRYFDNGTALVQMDHVVHLDQDNYNLGSFTFOATLLMDGRILFYKEIPVLVTOISSTNH 274
QY 251 PVKTGLSDAFMILNFPSPDVPESRRSIFEXHRIEIDPSKVTSMASAVETPLPTCLOHRSC 310
Db 275 PVKVGSLDAFVVHRIQIPNVRRTIYEHVRLQMSKITNISAVEMTPTLCLOFNRC 334
QY 311 DACMSSDLTFNCWCHVLRQCSGFDYRQWMDYGCQAEGRCMCEDFQDDHDSASPD 370
Db 335 GPCVSSQIGFNCWCKLQRCSSGFDHRRQDWDVSGCPESKEKMCENTPEVETSSRTT 394
QY 371 T--SFSPYDGLTTTS---SSLFIDSLTDEDTKLNYPAGGGLQ--NNLSPKTKGTPVHL 424
Db 395 TIGATTQFRVLTTTRRAVTSQFPTSLPTEDDTKIALHLKNGASTDDSAEKKGTLHA 454
QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPWPKMFKRSHPDHSTYAEV 484
Db 455 GLVIGLILVIVATALLVTVYMHHTPSAASIFFIERRPSRWPKMFKRSGHPAYAEV 514
QY 485 EPSGHEKEGFMEEQC 500
Db 515 EPVG-EKEGFIVSEQ 529

RESULT 10
ABB90734
ID ABB90734 standard; Protein: 529 AA.
XX AC ABB90734;
XX DT 30-MAY-2002 (first entry)
XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 200.
XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis.
XX OS Homo sapiens.
XX PN WO200210217-A2.
XX PD 07-FEB-2002.
XX PF 01-AUG-2001; 2001WO-US24031.
XX PR 02-AUG-2000; 2000US-222599P.
XX PR 11-AUG-2000; 2000US-224360P.
XX PR 11-APR-2001; 2001US-282850P.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2002-291856/33.
XX DR N-PSDB; ABL92088.

CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

XX XX Sequence 529 AA;

Query Match 48.1%; Score 1294; DB 22; Length 529;

Best Local Similarity 57.1%; Pred. No. 1e-115;

Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

Qy 72 LAMDTLPDNRTRVVED-NHSYVSRLYGSEPHSRLEWVDVAEANKRSQVKIHLNTHR 130
Db 95 LLLDGDQNNQTEEDTDHNYISRIYGPSDSASRLWVNDQMEKDKVKIHGILSNTHR 154
Qy 131 QASRVLSFDPPFYGHPLRQITATGGFIPMGDVIHRLMTATQYVAPLMANFNPGYSDNS 190
Db 155 QAARVNLSFDPPFYGHFLREITVATGGFIYTGVEVVRHMLTATQYIAPLMANFDPVSVRNS 214
Qy 191 TVVFDNGTVFVQWHDVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 215 TVRVFDNGTALVQWHDVHLQDNNYLGSTFQAALLMDGRIIFGYKEIPVLVTQISSTNH 274
Qy 251 PVKGLSDAFMILNPSDPVPSRRSIFEXHRIELDPKSVTSMASVETPLPTCLOHRSC 310
Db 275 PVKGLSDAFVVRHRIQIIPNVRRTIYEHVRVQLQMSKITINISAVEMTPLPTCLOFNR 334
Qy 311 DACSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGAQAEGRMCEDFQDEHDSASPD 370
Db 335 GPCVSSQIGFNCWCSKLQRCSSGFDHRQDWDVSGGPEESKEKMCENTPEVTSSTTT 394
Qy 371 T--SFSPYDGLTTS---SSLFTDLSLTEDDTKLNYPAGDGLQ--NNLSPKTKGTVPVHL 424
Db 395 TVGATTTQFRVLTTRRAVTSQFTSLPTEDDTKIALHLKONGASTDDSAEKKGGTLHA 454
Qy 425 GTIVGIVLAVLVAAILAGIYINGHPTSNAAFFIERRPHHPWAMPKFRSHDSTYAEV 484
Db 455 GLIIGILILVAVATAILVTVMYHHPTSAASIFFIERRPSRWPAKFRGSGHPAYAEV 514
Qy 485 EPSGHEKEGFMBAEQC 500
Db 515 EPVG-EKEGFIVSEQC 529

RESULT 12

AAM39068
ID AAM39068 standard; Protein; 529 AA.

XX XX

AC AAM39068;

XX XX

DT 22-OCT-2001 (first entry)

XX XX

DE Human polypeptide SEQ ID NO 2213.

XX XX

KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX XX

OS Homo sapiens.

XX XX

PN WO200153312-A1.

XX XX

PD 26-JUL-2001.

XX XX

PF 26-DEC-2000; 2000WO-US34263.

XX XX

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-052317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX XX

PA (HYSE-) HYSEQ INC.

XX XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX XX

DR WPI: 2001-442253/47.

XX N-PSDB; AAI58224.

PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX Example 4; SEQ ID NO 2213; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities such as: Immune system suppression,
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemia and
C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed
specification.

XX Sequence 529 AA;

Query Match 48.1%; Score 1294; DB 22; Length 529;

Best Local Similarity 57.1%; Pred. No. 1e-115;

Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

Qy 72 LAMDTLPDNRTRVVED-NHSYVSRLYGSEPHSRLEWVDVAEANKRSQVKIHLNTHR 130
Db 95 LLLDGDQNNQTEEDTDHNYISRIYGPSDSASRLWVNDQMEKDKVKIHGILSNTHR 154
Qy 131 QASRVLSFDPPFYGHPLRQITATGGFIPMGDVIHRLMTATQYVAPLMANFNPGYSDNS 190
Db 155 QAARVNLSFDPPFYGHFLREITVATGGFIYTGVEVVRHMLTATQYIAPLMANFDPVSVRNS 214
Qy 191 TVVFDNGTVFVQWHDVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 215 TVRVFDNGTALVQWHDVHLQDNNYLGSTFQAALLMDGRIIFGYKEIPVLVTQISSTNH 274
Qy 251 PVKGLSDAFMILNPSDPVPSRRSIFEXHRIELDPKSVTSMASVETPLPTCLOHRSC 310
Db 275 PVKGLSDAFVVRHRIQIIPNVRRTIYEHVRVQLQMSKITINISAVEMTPLPTCLOFNR 334
Qy 311 DACSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGAQAEGRMCEDFQDEHDSASPD 370
Db 335 GPCVSSQIGFNCWCSKLQRCSSGFDHRQDWDVSGGPEESKEKMCENTPEVTSSTTT 394
Qy 371 T--SFSPYDGLTTS---SSLFTDLSLTEDDTKLNYPAGDGLQ--NNLSPKTKGTVPVHL 424
Db 395 TVGATTTQFRVLTTRRAVTSQFTSLPTEDDTKIALHLKONGASTDDSAEKKGGTLHA 454
Qy 425 GTIVGIVLAVLVAAILAGIYINGHPTSNAAFFIERRPHHPWAMPKFRSHDSTYAEV 484
Db 455 GLIIGILILVAVATAILVTVMYHHPTSAASIFFIERRPSRWPAKFRGSGHPAYAEV 514

[illegible]

Db 275 PVKGLSDAFVYVHRIQQIPNVRRTIYEHVRELQMSKITNISAVEMTLPCTCLOQNR 334
 Qy 311 DACMSSDLTENCSCWCHVLRQCSGFDYRQEMWYDYGCAQAEGRMCEDFODEDHDGASPD 370
 Db 335 GPCVSSOIGFNCSCWCKLQRCSSGFDHRQDWDVDSGCPESKEKMCENTEPVETSSRTTT 394
 Qy 371 T--SFSYDGLTTS--SSLEFIDSLTTEDDTKLNYPYAGDGLQ--NNLSPKTKGTPVHL 424
 Db 395 TVGATTTQFRVLTTRAVTSQPTSLPTEDDTKIALHLKNDGASDTSAAEKKGGTLHA 454
 Qy 425 GTIVGIVLAVLLAAIILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHDPDHYAEV 484
 Db 455 GLIIGILLVIVATAILVTVYVYHHTSAASIFFIERRSRWPAKFRGRSGHPAYAEV 514
 Qy 485 EPSGHERKEGFMEAEQC 500
 Db 515 EPVG-EKEGFIVSEQ 529

RESULT 14
 AAG64527
 ID AAG64527 standard; Protein; 425 AA.
 XX
 AC AAG64527;
 XX
 DT 04-OCT-2001 (first entry)
 XX
 DE Human polypeptide 784_3137 contig SEQ ID NO 2.
 XX
 KW Human; antisense-therapy; gene-therapy; diagnostic; forensic;
 KW gene mapping.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH Misc-difference 287
 FT /note= "Encoded by TCCTT"
 FT
 FT Misc-difference 293
 FT /note= "Encoded by CCATAG"
 FT
 FT Misc-difference 302
 FT /note= "Encoded by TCCTAA"
 FT
 FT Misc-difference 307
 FT /note= "Encoded by GA"
 FT
 FT
 PN WO200152616-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 22-DEC-2000; 2000WO-US35190.
 XX
 PR 23-DEC-1999; 99US-0471275.
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-451909/48.
 DR
 DR N-PSDB; AAH75398.
 XX
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 XX
 XX Claim 1; Page 15; 135pp; English.
 PS
 CC The invention relates to an isolated human polynucleotide (AAH75398)
 CC encoding a novel polypeptide (AAG64527) useful in antisense-therapy and
 CC gene-therapy, in diagnostics, forensics, gene mapping and identification
 CC of mutations responsible for genetic disorders and other traits.
 CC Polynucleotide sequences with potential homology were also identified
 CC (AAH93283-AAH93356).
 CC
 XX

SQ Sequence 425 AA;
 Query Match 47.4%; Score 1276; DB 22; Length 425;
 Best Local Similarity 57.7%; Pred. No. 4e-114;
 Matches 248; Conservative 64; Mismatches 106; Indels 12; Gaps 5;
 Qy 78 PNRTRRVVDNHSYVSRUYGSPSEHRSRLWVDVAEANSRQVKIHTILSNTHROASRVVL 137
 Db 1 PRVRPRVRTD-RNYIYISRIYGSDSASRLWVNDQMEKDKVKIHILSNTHROAARVNL 59
 Qy 138 SFDFFPYGHPRLRQITATCGFIFMGDVIHRMLTATQYVAPLMANPNPGYSNDSTVYEDN 197
 Db 60 SEDFFPYGHFLREITVATGFGFIYTGCVHRLMTATQYIAPLMANEDPVSYSRNSTVRYEDN 119
 Qy 198 GTVFVQVQNDHVYLGWEDKGSFTQAAALHHDGRIVFAYKEIPMSYPEISSOSHPPVKTGLS 257
 Db 120 GTALVQVQNDHVYLGWEDKGSFTQAAALHHDGRIVFAYKEIPMSYPEISSOSHPPVKTGLS 179
 Qy 258 DAFMILNPSDPVPESRRRSIFEYHRIELDPKSVTSMASAVEFTPLPTCLOHRSQDCAACMSD 317
 Db 180 DAFVVRHRIQQIPNVRRTIYEHVRELQMSKITNISAVEMTLPCTCLOHRSQDCAACMSD 239
 Qy 318 LTFNCSCWCHVLRQCSGFDYRQEMWYDYGCAQAEGRMCEDFODEDHDGASPT 371
 Db 240 IGFCNCSKLRQCSGFDYRQEMWYDYGCAQAEGRMCEDFODEDHDGASPT 299
 Qy 372 SFSYDGLTTS--SSLEFIDSLTTEDDTKLNYPYAGDGLQ--NNLSPKTKGTPVHLGTIVGI 430
 Db 300 SGLPPEDAVT---SOFPTSLPTEDDTKIALHLKNDGASDTSAAEKKGGTLHAGLIVGI 356
 Qy 431 VLAVLLVAAIILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHDPDHYAEVPSGHE 490
 Db 357 LILVIVATAILVTVYVYHHTSAASIFFIERRSRWPAKFRGRSGHPAYAEVPEVG-E 415
 Qy 491 KEGFMEAEQC 500
 Db 416 KEGFIVSEQ 425

RESULT 15
 AAB85399
 ID AAB85399 standard; Protein; 425 AA.
 XX
 AC AAB85399;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Stem cell growth factor-like polypeptide fragment.
 XX
 KW Stem cell growth factor-like polypeptide; leukemia; hemophilia; human;
 KW degenerative disease; Alzheimer's disease; nutritional supplement;
 KW cytotatic; nootropic; neuroprotective; hemostatic; antisense-therapy;
 KW gene-therapy; cell proliferation; stem cell growth factor.
 XX
 OS Homo sapiens.
 XX
 PN WO200153500-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 23-DEC-2000; 2000WO-US35260.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 07-APR-2000; 2000US-0545714.
 PR 11-APR-2000; 2000US-0547358.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Labat I, Tang YT, Drmanac RT, Liu C, Lee J, Mize NK, Childs J;
 PI Chao C;
 XX
 XX WPI; 2001-451909/48.
 DR
 XX

PT Isolated polypeptide with stem cell growth factor-like activity for
PT treatment of leukemia, hemophilia, and degenerative diseases like
PT Alzheimer's disease and to generate new tissues and organs -
XX
XX
XX Claim 10; Page 147-149; 154pp; English.
XX
XX The invention provides novel human stem cell growth factor-like
XX polypeptides and polynucleotides encoding them. The polypeptides having
XX stem cell growth factor-like activity, can be expressed by standard
XX recombinant methodology. The polynucleotides and polypeptides can be
XX used to induce differentiation of embryonic and adult stem cells to give
XX rise to different cell types. They may also be used in the treatment of
XX leukemia, hemophilia, and degenerative diseases like Alzheimer's disease.
XX They may also be utilized to generate new tissues and organs that may aid
XX patients in need of transplants. They can also be used as nutritional
XX supplements. The present sequence represents a stem cell growth factor-
XX like polypeptide fragment.
SQ Sequence 425 AA;

Query Match 47.4%; Score 1276; DB 22; Length 425;
Best Local Similarity 57.7%; Pred. NO. 4e-114;
Matches 248; Conservative 64; Mismatches 106; Indels 12; Gaps 5;

QY 78 PDNRTRVVEDNHSYVSRLYGSEPHSRELWVDVAEANRFSQVKIHTILSNTHRQASRVVL 137
Db 1 PVRVRVRTD-HNYIYISRIYGPDSASRDLWNIDQMEKDKYKIHGILSNTHRQAARVNL 59
QY 138 SFDFPFYGHPLRQIITATGGTIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTWVYFDN 197
Db 60 SFDFPFYGHFLREITVATGGTIFMGDVIHRMLTATQYVAPLMAFNPGYSDNSTWVYFDN 119
QY 198 GTVFWQNDHYVLOQWEDKSGFTQAAHLHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 257
Db 120 GTALVVQNDHYVLOQWEDKSGFTQAAHLHDGRIVFAYKEIPMSVPEISSQHPVKTGLS 179
QY 258 DAFMLNPSDPVPSRRRSIFEHRIELDPKVTSMASAVEFTPLPTCLOHRSKCDACMSD 317
Db 180 DAFVVVHRIQIPNVRRTIYEHVRELQMSKIINISAVEMTPLTCLQNRGCPVSSQ 239
QY 318 LTFNCSWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCED-----FQDEHDHDSASPD 371
Db 240 LTFNCSWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCED-----FQDEHDHDSASPD 299
QY 372 SFSPYDGLTTSSTSLFDTLTTEDDTKLNYPYAGDGLQ-NLSPKTKTPTVHLGTIVGI 430
Db 300 SGLPPEDAVT---SQPTSLPTEDDTKLNYPYAGDGLQ-NLSPKTKTPTVHLGTIVGI 356
QY 431 VLAVLLAAIILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAEVEPSGHE 490
Db 357 LILVLIVATAILVTVYMYHHPTSAASIFFIERRPHHPAMKFRSHPDHSTYAEVEPSGHE 415
QY 491 KEGFWEAEQC 500
Db 416 KEGFIVSEQC 425

Search completed: April 22, 2003, 16:06:33
Job time : 81 secs

PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234597.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.

PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-483426/52.
XX N-PSDB; AAK61650.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Claim 11; SEQ ID NO 16462; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins, and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 205 AA;

Query Match 21.6%; Score 108; DB 22; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-100;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 KEIPMSVPEISSQHPVKVTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSA 295
|||||
Db 58 KEIPMSVPEISSQHPVKVTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSA 117
|||||
QY 296 VEFTPLPTCLOHRSKCDACMSDDLTFNCWSCHVLQRCSSGFDYRQEMW 343
|||||
Db 118 VEFTPLPTCLOHRSKCDACMSDDLTFNCWSCHVLQRCSSGFDYRQEMW 165
|||||

RESULT 7
AAW58986
ID AAW58986 standard; Protein; 108 AA.
XX
AC AAW58986;
XX
DF 11-SEP-1998 (first entry)
XX
XX Homo sapiens adult brain clone CC194_4 encoded protein.
DE
XX adult; brain; cDNA library; clone CC194_4; secreted protein
KW autoimmune disease; anti-inflammatory; immune; stimulation
KW suppression.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 40 /note= "undefined amino acid, encoded by AMT"

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 CC osteoparathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus, lupus
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 400 AA;

Query Match 74.2%; Score 371; DB 21; Length 400;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELMLLVLRARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPR 60
 DB 29 MRGELMLLVLRARALSPQAGHDEGPGSGWAAKGTVRGNRRARESPGHVSEPR 88
 QY 61 TQLSDQLGGTGLAMDTLPNRRTRVEDNHSYVSRLYGSPHSELVDVAEANKRSQVK 120
 DB 89 TQLSDQLGGTGLAMDTLPNRRTRVEDNHSYVSRLYGSPHSELVDVAEANKRSQVK 148
 QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
 DB 149 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 208
 QY 181 NFNPYSDNSTVYFNGTGVVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
 DB 209 NFNPYSDNSTVYFNGTGVVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 268
 QY 241 SVPEISSQHPVKITGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 300
 DB 269 SVPEISSQHPVKITGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTP 328
 QY 301 LPTCLQHRSCDACMSSDLTFNCWSCHVLQRCSSGFDYRQEWMDYGCAGEGRMCEDFQ 360
 DB 329 LPTCLQHRSCDACMSSDLTFNCWSCHVLQRCSSGFDYRQEWMDYGCAGEGRMCEDFQ 388
 QY 361 DEHDASAPDT 371
 DB 389 DEHDASAPDT 399

RESULT 4
 AAB85400
 ID AAB85400 standard; Protein; 431 AA.
 XX
 AC AAB85400;

17-SEP-2001 (first entry)
 XX Tumour endothelial marker 7 precursor protein.
 DE Stem cell growth factor-like polypeptide; leukemia; hemophilia; human;
 XX degenerative disease; Alzheimer's disease; nutritional supplement;
 KW cytotstatic; nootropic; neuroprotective; hemostatic; antisense-therapy;
 KW gene-therapy; tumour endothelial marker 7 precursor protein.
 XX
 OS Homo sapiens.

XX WO200153500-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 23-DEC-2000; 2000WO-US35260.
 PF
 XX 21-JAN-2000; 2000US-0488725.
 PR 07-APR-2000; 2000US-0545714.
 PR 11-APR-2000; 2000US-0547358.
 XX (HYSE-) HYSEQ INC.
 PA Labat I, Tang YT, Drmanac RT, Liu C, Lee J, Mize NK, Childs J;
 PI Chao C;
 PI WPI: 2001-451909/48.
 DR
 XX Isolated polypeptide with stem cell growth factor-like activity for
 PT treatment of leukemia, hemophilia, and degenerative diseases like
 PT Alzheimer's disease and to generate new tissues and organs -
 XX
 PS Example 4; Page 149-150; 154pp; English.
 XX
 CC The invention provides novel human stem cell growth factor-like
 CC polypeptides and polynucleotides encoding them. The polypeptides having
 CC stem cell growth factor-like activity, can be expressed by standard
 CC recombinant methodology. The polynucleotides and polypeptides can be
 CC used to induce differentiation of embryonic and adult stem cells to give
 CC rise to different cell types. They may also be used in the treatment of
 CC leukemia, hemophilia, and degenerative diseases like Alzheimer's disease.
 CC They may also be utilized to generate new tissues and organs that may aid
 CC patients in need of transplants. They can also be used as nutritional
 CC supplements. The present sequence represents a tumour endothelial marker
 CC 7 precursor protein, homologous to a stem cell growth factor-like
 CC polypeptide.
 XX
 SQ Sequence 431-AA;

Query Match 54.2%; Score 271; DB 22; Length 431;
 Best Local Similarity 100.0%; Pred. No. 5.3e-264;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 LAMDTLPDNRTRVEDNHSYVSRLYGSPHSELVDVAEANKRSQVKIHTILSNTHRQ 131
 DB 1 LAMDTLPDNRTRVEDNHSYVSRLYGSPHSELVDVAEANKRSQVKIHTILSNTHRQ 60
 QY 132 ASRVVLSDFRPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNST 191
 DB 61 ASRVVLSDFRPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPGYSDNST 120
 QY 192 VVYFDNGTGVVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 251
 DB 121 VVYFDNGTGVVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHP 180
 QY 252 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTPCLQHRSCD 311
 DB 181 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTPCLQHRSCD 240
 QY 312 ACMSSDLTFNCWSCHVLQRCSSGFDYRQEW 342
 DB 241 ACMSSDLTFNCWSCHVLQRCSSGFDYRQEW 271

RESULT 5
 ABB90077
 ID ABB90077 standard; Protein; 146 AA.
 XX
 AC ABB90077;
 XX 24-MAY-2002 (first entry)
 DT
 XX Human polypeptide SEQ ID NO 2453.
 DE

ID AC ABB90723 standard; Protein; 1002 AA.
XX AC ABB90723;
XX DT 30-MAY-2002 (first entry)
XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.
XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antitumorigenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis.
XX OS Homo sapiens.
XX PN WO200210217-A2.
XX PD 07-FEB-2002.
XX PF 01-AUG-2001; 2001WO-US24031.
XX PR 02-AUG-2000; 2000US-222599P.
XX PR 11-AUG-2000; 2000US-224360P.
XX PR 11-APR-2001; 2001US-282850P.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI St Croix B, Kinzler KW, Vogelstein B;
XX DR WPI; 2002-291856/33.
XX DT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth -
XX Disclosure; Page 125-128; 331pp; English.
XX CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in
CC subjects bearing a vascularised tumour, polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
CC and pan-endothelial markers (PEM) ABL91903-ABL91995.
XX SQ Sequence 1002 AA;
Query Match 100.0%; Score 500; DB 23; Length 1002;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGRNRRARESPGHVSPDR 60
Db 503 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGRNRRARESPGHVSEPR 562
Qy 61 TOLSDGLGGTAMDTPDNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAENRSQVK 120
Db 563 TOLSDGLGGTAMDTPDNTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAENRSQVK 622
Qy 121 IHTILSNTHRAQSRVLSFDPFPGHPLRQITATGTFIEMGDVTHRLMTATQVAPLMA 180
Db 623 IHTILSNTHRAQSRVLSFDPFPGHPLRQITATGTFIEMGDVTHRLMTATQVAPLMA 682
Qy 101 NFNPYSDNSTVYVFDNGTVEVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 683 NFNPYSDNSTVYVFDNGTVEVQWQDHVYLGQWEDKGSFTFQAALHHDGRIVFAYKEIPM 742

Qy 241 SVPELSSQHPVKTCLSDAFMILNPSDPVPSRRRSIFEXHRIELDFSKVTSMSAVEFTP 300
Db 743 SVPELSSQHPVKTCLSDAFMILNPSDPVPSRRRSIFEXHRIELDFSKVTSMSAVEFTP 802
Qy 301 LPTCLQHRSCDACMSSDLTFCNSCHVLQRCSSGDFRYROEWMYDYGCAQEAEGRMCEDFQ 360
Db 803 LPTCLQHRSCDACMSSDLTFCNSCHVLQRCSSGDFRYROEWMYDYGCAQEAEGRMCEDFQ 862
Qy 361 DEDHDSASPTSFSPYDGLTFTSSSIFIDSLTTEDDTKLNPYAGSGDGLQNNLSPKTKGT 420
Db 863 DEDHDSASPTSFSPYDGLTFTSSSIFIDSLTTEDDTKLNPYAGSGDGLQNNLSPKTKGT 922
Qy 421 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAIFFERRPHHPWPAKFRSHPDHST 480
Db 923 PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAAIFFERRPHHPWPAKFRSHPDHST 982
Qy 481 YAEVPSGHEKEGFMEEQC 500
Db 983 YAEVPSGHEKEGFMEEQC 1002
RESULT 3
AAB43131
ID AAB43131 standard; Protein; 400 AA.
XX AC AAB43131;
XX DT 08-FEB-2001 (first entry)
XX DE Human ORFX ORF2895 polypeptide sequence SEQ ID NO:5790.
XX KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antineumatic; antichyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX OS Homo sapiens.
XX PN WO200058473-A2.
XX PD 05-OCT-2000.
XX PF 31-MAR-2000; 2000WO-US08621.
XX PR 31-MAR-1999; 99US-0127607.
XX PR 02-APR-1999; 99US-0127636.
XX PR 05-APR-1999; 99US-0127728.
XX PR 30-MAR-2000; 2000US-0540763.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI; 2000-602362/57.
XX DR N-PSDB; AAC77340.
XX PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX Claim 11; Page 4955; 5507pp; English.

960 6 1.2 233 21 AAG26203
 961 6 1.2 233 21 AAG39338
 962 6 1.2 233 21 AAG52988
 963 6 1.2 233 21 ABG16403
 964 6 1.2 233 21 AAM40813
 965 6 1.2 233 22 AAB79268
 966 6 1.2 233 22 ABP26839
 967 6 1.2 233 20 AAY34823
 968 6 1.2 235 23 ABB08196
 969 6 1.2 236 15 AAB34225
 970 6 1.2 236 22 ABB68490
 971 6 1.2 236 22 ABG20233
 972 6 1.2 236 22 ABB12038
 973 6 1.2 236 22 AAM25821
 974 6 1.2 236 23 ABB45660
 975 6 1.2 237 21 AAG36694
 976 6 1.2 237 22 ABB67569
 977 6 1.2 237 23 ABB89553
 978 6 1.2 237 23 AAM50929
 979 6 1.2 238 21 AAB58791
 980 6 1.2 239 21 AAG07150
 981 6 1.2 239 21 AAG53553
 982 6 1.2 239 22 AAG55689
 983 6 1.2 240 22 AAB96797
 984 6 1.2 240 23 ABB92402
 985 6 1.2 241 22 AAG65077
 986 6 1.2 241 22 AAG03626
 987 6 1.2 241 22 AAG28310
 988 6 1.2 242 21 AAG26202
 989 6 1.2 243 21 AAB58248
 990 6 1.2 244 21 AAY81721
 991 6 1.2 244 23 ABB93605
 992 6 1.2 245 10 AAP90386
 993 6 1.2 245 22 ABB65303
 994 6 1.2 245 22 ABB10688
 995 6 1.2 245 22 AAU31134
 996 6 1.2 245 22 AAG90194
 997 6 1.2 246 20 AAY14201
 998 6 1.2 246 21 AAG13702
 999 6 1.2 247 21 AAG42005
 1000 6 1.2 247 21 AAG52568

ALIGNMENTS

RESULT 1
 ABB90749
 ID ABB90749 standard; Protein: 500 AA.

XX AC ABB90749;
 XX AC
 XX AC
 DT 30-MAY-2002 (first entry)

XX Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.

DE Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neovascularisation; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.

XX Homo sapiens.

XX OS
 XX PN WO200210217-A2.

XX 07-FEB-2002.

XX 01-AUG-2001; 2001WO-US24031.

XX 02-AUG-2000; 2000US-222599P.

XX 11-AUG-2000; 2000US-224360P.

XX 11-APR-2001; 2001US-282850P.

XX (UYJO) UNIV JOHNS HOPKINS.
 PA St Croix B, Kinzler KW, Vogelstein B;
 XX WPI; 2002-291856/33.
 DR N-PSDB; ABL92103.
 DR

PT An isolated molecule comprising an antibody variable region which
 specifically binds to an extracellular domain of a tumor endothelial
 marker (TEM) protein, useful for inhibiting tumor growth -
 Claim 1; Page 206-207; 33pp; English.

CC The invention relates to an isolated molecule comprising an antibody
 variable region which specifically binds to an extracellular domain of a
 tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neovascularisation in
 subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.

XX Sequence 500 AA;

Query Match 100.0%; Score 500; DB 23; Length 500;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELLLVLRRAALSPQAGHDEGPGSCAAKGTVRGNRRARSPGHVSEPD 60
 Db 1 MRGELLLVLRRAALSPQAGHDEGPGSCAAKGTVRGNRRARSPGHVSEPD 60
 Qy 61 TQLSODLGGGTLMADTLPDNTRVVDNHNHYSYVSLYGPSPHRELWVDVAEANSQVK 120
 Db 61 TQLSODLGGGTLMADTLPDNTRVVDNHNHYSYVSLYGPSPHRELWVDVAEANSQVK 120
 Qy 121 IHTILSNTHROASRVLSDFPFYCHPLRQITATGGFIEMGDVTHRLMTATQVAPLMA 180
 Db 121 IHTILSNTHROASRVLSDFPFYCHPLRQITATGGFIEMGDVTHRLMTATQVAPLMA 180
 Qy 181 NFNPYSDNSTVWYFDNGTGVFVQWHDVYVLOGWEDKGSFTFQAAALHHDGRIVFAYKEIPM 240
 Db 181 NFNPYSDNSTVWYFDNGTGVFVQWHDVYVLOGWEDKGSFTFQAAALHHDGRIVFAYKEIPM 240
 Qy 241 SVPEISSQHPVKTKGLSDAFMLNLPSPDPESRRRSIFEYHRIELDPKVTMSAVEETP 300
 Db 241 SVPEISSQHPVKTKGLSDAFMLNLPSPDPESRRRSIFEYHRIELDPKVTMSAVEETP 300
 Qy 301 LPTCLQHRSCDACMSDDLTFNCWCHVLRQCSGDFRQEWMDYGCQAEGRMCEDFQ 360
 Db 301 LPTCLQHRSCDACMSDDLTFNCWCHVLRQCSGDFRQEWMDYGCQAEGRMCEDFQ 360
 Qy 361 DEDHDSASPDTSFSPYDGLTTSLSLFDLSITTEDDTKLNYPAGDGLQNNLSPKTKGT 420
 Db 361 DEDHDSASPDTSFSPYDGLTTSLSLFDLSITTEDDTKLNYPAGDGLQNNLSPKTKGT 420
 Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTISNAALFFIERPPHHWPAKFRSHPDHST 480
 Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTISNAALFFIERPPHHWPAKFRSHPDHST 480
 Qy 481 YAEVPSGHEKEGFMEEQEC 500
 Db 481 YAEVPSGHEKEGFMEEQEC 500

RESULT 2
 ABB90723

814	1.2	193	22	AAM15133	Peptide #1567 enco	887	6	1.2	214	22	AAG90925	C glutamicum prote
815	1.2	193	22	AAM27588	Peptide #1625 enco	888	6	1.2	214	23	ABB77890	Amino acid sequenc
816	1.2	193	22	AAM20874	Peptide #1556 enco	889	6	1.2	215	21	AAB54208	Human pancreatic c
817	1.2	193	23	ABG36943	Human peptide enco	890	6	1.2	215	21	AAG04896	Arabidopsis thalia
818	1.2	193	23	ABB47646	Listeria monocytog	891	6	1.2	215	21	AAG50849	Arabidopsis thalia
819	1.2	194	20	AAI37221	Amino acid sequenc	892	6	1.2	215	22	AAG66289	Human tankyrase2 c
820	1.2	194	21	AAG07582	Arabidopsis thalia	893	6	1.2	215	23	ABB77893	Amino acid sequenc
821	1.2	195	21	AAG07313	Arabidopsis thalia	894	6	1.2	216	23	AAG51946	Arabidopsis thalia
822	1.2	195	22	ABH80090	Corynebacterium gl	895	6	1.2	216	23	ABP29667	Streptococcus poly
823	1.2	195	22	ABH41856	Human ovarian anti	896	6	1.2	216	23	ABB89202	Human polypeptide
824	1.2	195	23	ABB06799	Human nPCR-Seq101	897	6	1.2	217	21	AAG17021	Arabidopsis thalia
825	1.2	196	18	AAM26746	S. carnosus nitrat	898	6	1.2	218	22	ABB66933	Drosophila melanog
826	1.2	196	21	AAG17022	Arabidopsis thalia	899	6	1.2	218	22	AAG69760	Escherichia coli U
827	1.2	196	21	AAG51947	Arabidopsis thalia	900	6	1.2	218	23	AAU11282	Human testicular t
828	1.2	196	22	AAM29434	Human G protein-co	901	6	1.2	219	22	ABB66771	Drosophila melanog
829	1.2	196	23	ABG60722	Novel G protein co	902	6	1.2	219	23	AAU92997	Drosophila melanog
830	1.2	197	23	ABP29524	Streptococcus poly	903	6	1.2	220	22	ABB68171	Propionibacterium
831	1.2	197	23	AAE18281	Bovine fertility a	904	6	1.2	220	22	AAU42147	Novel human diagno
832	1.2	197	23	AAU11516	Bovine fertility a	905	6	1.2	221	22	ABG23687	C glutamicum prote
833	1.2	198	21	AAB42354	Bovine fertility-a	906	6	1.2	221	22	ABP41862	Human ovarian anti
834	1.2	198	22	ABB31735	Human ORFX ORF2118	907	6	1.2	221	23	ABP40139	Staphylococcus epi
835	1.2	198	22	ABB36957	Peptide #4386 enco	908	6	1.2	221	23	ABP27808	Streptococcus poly
836	1.2	198	22	ABB22271	Peptide #4463 enco	909	6	1.2	222	12	AAR13943	Calcium channel ga
837	1.2	198	22	AAU25706	Protein #4270 enco	910	6	1.2	222	20	AAW78210	Human secreted pro
838	1.2	198	22	AAU57690	G protein-coupled	911	6	1.2	222	21	AAW54894	Human secreted pro
839	1.2	198	22	AAU70097	Human brain expres	912	6	1.2	222	21	AAU54894	Arabidopsis thalia
840	1.2	198	22	AAU70097	Human bone marrow	913	6	1.2	222	22	AAU45233	Propionibacterium
841	1.2	198	22	AAU71924	Peptide #4358 enco	914	6	1.2	222	22	ABG27005	Novel human diagno
842	1.2	198	22	AAU30436	Peptide #4473 enco	915	6	1.2	222	22	AAU73292	Murine TSG-like pr
843	1.2	198	22	AAU05574	Peptide #4256 enco	916	6	1.2	222	23	AAU75170	Murine BMP polypept
844	1.2	198	23	ABG39732	Human peptide enco	917	6	1.2	222	23	AAU32112	Mouse BMP polypept
845	1.2	199	18	AAW34131	Streptococcus pneu	918	6	1.2	223	19	AAW70591	A novel human cyto
846	1.2	199	18	AAW34131	Dirofilaria immiti	919	6	1.2	223	20	AAU28504	Human growth facto
847	1.2	199	19	AAW71493	Helicobacter polyp	920	6	1.2	223	20	AAU28504	HGP44 Human Growth
848	1.2	199	22	AAU92802	S. pneumoniae hist	921	6	1.2	223	22	ABB67311	Drosophila melanog
849	1.2	199	22	ABP38980	H. pylori HPC134 p	922	6	1.2	223	22	ABB68460	Human membrane or
850	1.2	199	23	ABP47696	Staphylococcus epi	923	6	1.2	223	22	ABP1856	Human D-SLAM extra
851	1.2	200	19	AAU11076	Listeria monocytog	924	6	1.2	223	23	ABP42145	Human ovarian anti
852	1.2	200	22	AAU81650	H. pylori ORF hp4e	925	6	1.2	223	23	ABP42145	Human ORFX ORF997
853	1.2	200	22	AAU82074	S. epidermidis ope	926	6	1.2	224	21	ABP41233	Novel human diagno
854	1.2	200	21	AAU82074	S. epidermidis ope	927	6	1.2	224	22	ABG12473	Human novel secret
855	1.2	201	21	AAU83339	Arabidopsis thalia	928	6	1.2	224	22	AAU16512	Human ORFX ORF3031
856	1.2	201	21	AAU83339	Arabidopsis thalia	929	6	1.2	226	21	AAU18451	A human TANGO 262
857	1.2	201	22	ABG26652	Human tonka protel	930	6	1.2	226	21	AAU18451	A human TANGO 262
858	1.2	201	23	AAU11517	Novel human diagno	931	6	1.2	226	21	AAU18467	A human TANGO 262
859	1.2	201	23	AAU11517	Human fertility-as	932	6	1.2	226	21	AAU18467	A human TANGO 262
860	1.2	202	21	AAU38453	Fragment of human	933	6	1.2	226	21	AAU18470	A murine TANGO 262
861	1.2	202	21	AAU75719	Neisseria gonorrhoe	934	6	1.2	226	21	AAU18471	A murine TANGO 262
862	1.2	202	22	ABG07421	Novel human diagno	935	6	1.2	226	21	AAU18472	A murine TANGO 262
863	1.2	204	23	ABP38988	Staphylococcus epi	936	6	1.2	226	21	AAU25758	Human secreted pro
864	1.2	205	22	AAU41633	Propionibacterium	937	6	1.2	226	21	AAU25758	Human secreted pro
865	1.2	205	22	AAU62716	Propionibacterium	938	6	1.2	226	22	ABB64681	Drosophila melanog
866	1.2	206	18	AAU55249	H. pylori ORF 05cp	939	6	1.2	226	22	AAU29084	Human PRO polypept
867	1.2	206	18	AAU17978	dTPD-4-keto-6-deox	940	6	1.2	226	22	AAU29084	S. avermitilis ORF
868	1.2	206	21	AAU05055	Arabidopsis thalia	941	6	1.2	226	22	AAU25344	Human PRO1079 (UNQ
869	1.2	206	21	AAU74875	Arabidopsis thalia	942	6	1.2	226	22	AAU75372	Secreted protein #
870	1.2	206	22	AAU33169	C glutamicum prote	943	6	1.2	226	23	ABB93475	Human secreted pro
871	1.2	206	22	AAU66291	Human tankyrase2 c	944	6	1.2	226	23	ABB93475	Human angiogenesis
872	1.2	206	23	ABP39084	Streptococcus pneu	945	6	1.2	226	23	ABB84869	Human PRO1079 prot
873	1.2	207	23	AAU99067	Human secreted pro	946	6	1.2	227	20	AAU41330	Human secreted pro
874	1.2	207	21	AAU91605	S. epidermidis ope	947	6	1.2	227	22	ABG20234	Novel human diagno
875	1.2	209	22	AAU81797	S. epidermidis ope	948	6	1.2	227	23	ABP26653	Streptococcus poly
876	1.2	209	22	AAU82571	Drosophila melanog	949	6	1.2	228	21	AAG23907	Arabidopsis thalia
877	1.2	210	22	ABH58697	Novel human diagno	950	6	1.2	228	21	AAG56586	Arabidopsis thalia
878	1.2	210	22	ABG15061	Mouse osteoblast d	951	6	1.2	228	22	AAU05350	Mouse surface glyco
879	1.2	212	21	AAU12480	Arabidopsis thalia	952	6	1.2	228	23	ABP72360	Murine protein iso
880	1.2	212	21	AAU36695	Streptococcus poly	953	6	1.2	229	11	AAU05699	Preprolactin from
881	1.2	212	23	ABP28918	Pheromone receptor	954	6	1.2	229	22	AAU31659	Novel human secret
882	1.2	213	13	AAU27878	Arabidopsis thalia	955	6	1.2	229	23	AAU83233	Novel secreted pro
883	1.2	213	23	AAU05054	Human polypeptide	956	6	1.2	230	22	AAU52576	Propionibacterium
884	1.2	213	23	ABP90201	Human secreted pro	957	6	1.2	232	21	AAG07151	Arabidopsis thalia
885	1.2	214	21	AAU91493	Drosophila melanog	958	6	1.2	232	21	AAG13703	Arabidopsis thalia
886	1.2	214	22	ABB65814		959	6	1.2	232	21	AAG53554	Arabidopsis thalia

668	6	1.2	146	22	AAU56080	Propionibacterium	741	6	1.2	167	21	AAG14830	Arabidopsis thalia
669	6	1.2	147	22	AAU22335	Human cardiovascular	742	6	1.2	167	22	AU48946	Propionibacterium
670	6	1.2	147	23	ABB53904	Lactococcus lactis	743	6	1.2	168	23	ABP89999	Human polypeptide
671	6	1.2	147	23	ABB55165	Lactococcus lactis	744	6	1.2	170	21	AAG14829	Arabidopsis thalia
672	6	1.2	148	13	AAR36410	Human phospholipase	745	6	1.2	170	22	AAU41312	Propionibacterium
673	6	1.2	148	16	AAR36410	Human phospholipase	746	6	1.2	170	22	AAU23046	Novel human enzyme
674	6	1.2	148	16	AAR36410	Human phospholipase	747	6	1.2	170	22	AG93097	C glutamic prote
675	6	1.2	148	22	AAU94451	Human protein sequ	748	6	1.2	170	22	ABP90048	Human polypeptide
676	6	1.2	148	22	AAU78667	Human phospholipase	749	6	1.2	170	23	ABP90048	Human polypeptide
677	6	1.2	148	23	AAU78668	Human phospholipase	750	6	1.2	172	21	AAG12942	Arabidopsis thalia
678	6	1.2	149	22	AAU89163	Human immune/haema	751	6	1.2	172	21	AAG36892	Arabidopsis thalia
679	6	1.2	150	20	AAU36774	Chlamydia trachoma	752	6	1.2	172	22	AAU13544	Human polypeptide
680	6	1.2	150	21	AAG10880	Arabidopsis thalia	753	6	1.2	172	23	ABP42854	Human ovarian anti
681	6	1.2	150	22	ABP71453	Drosophila melanog	754	6	1.2	172	23	ABP42854	Human OREX protein
682	6	1.2	151	22	AAU32409	Novel human secret	755	6	1.2	172	23	ABP42854	Human OREX protein
683	6	1.2	151	23	ABP53870	Lactococcus lactis	756	6	1.2	173	21	AAG15810	Arabidopsis thalia
684	6	1.2	152	22	AAU23400	Novel human enzyme	757	6	1.2	173	23	ABP29065	Streptococcus poly
685	6	1.2	153	10	AAU90380	Sequence of sorbin	758	6	1.2	174	19	ABP20786	Human neurofilamen
686	6	1.2	153	22	AAU47278	Propionibacterium	759	6	1.2	174	22	AAU71930	Human bone marrow
687	6	1.2	153	22	ABG01976	Novel human diagno	760	6	1.2	175	21	ABP32725	Eucalyptus grandis
688	6	1.2	153	22	AAE13103	Human phospholipase	761	6	1.2	175	21	AAG04897	Arabidopsis thalia
689	6	1.2	153	22	AAE13103	Human phospholipase	762	6	1.2	175	21	AAG04897	Arabidopsis thalia
690	6	1.2	153	23	ABP33830	Amino acid sequenc	763	6	1.2	175	23	ABP33830	Mouse ztnr12 prot
691	6	1.2	154	20	AAU81994	Tobacco trehalase	764	6	1.2	175	23	ABP33830	Murine BAPF recept
692	6	1.2	155	22	AAU50821	Propionibacterium	765	6	1.2	176	21	ABP33830	Human polypeptide
693	6	1.2	155	22	AAU50821	C glutamic prote	766	6	1.2	176	21	ABP33830	Eucalyptus grandis
694	6	1.2	156	21	AAU50821	Human pancreatic c	767	6	1.2	176	21	ABP33830	Neisseria meningit
695	6	1.2	156	21	AAU50821	Arabidopsis thalia	768	6	1.2	176	21	ABP33830	Neisseria meningit
696	6	1.2	156	22	AAU50821	Rat EST encoded pr	769	6	1.2	176	21	ABP33830	Human polypeptide
697	6	1.2	156	23	ABP25729	Streptococcus poly	770	6	1.2	177	23	ABP25729	Amino acid sequenc
698	6	1.2	157	21	AAU16353	Eucalyptus grandis	771	6	1.2	178	20	ABP25729	Novel human diagno
699	6	1.2	157	21	AAU16353	Zea mays protein f	772	6	1.2	178	22	ABP25729	Novel human diagno
700	6	1.2	157	22	AAU16353	Human polypeptide	773	6	1.2	179	21	ABP25729	Human expressed po
701	6	1.2	157	22	AAU16353	Human polypeptide	774	6	1.2	179	22	ABP25729	Novel human enzyme
702	6	1.2	158	21	AAU16353	Human tankyrase2 c	775	6	1.2	180	21	ABP25729	Human 54372 domain
703	6	1.2	158	21	AAU16353	Human tankyrase2 c	776	6	1.2	180	21	ABP25729	Arabidopsis thalia
704	6	1.2	158	22	AAU16353	Arabidopsis thalia	777	6	1.2	181	22	ABP25729	Arabidopsis thalia
705	6	1.2	158	22	AAU16353	Arabidopsis thalia	778	6	1.2	181	22	ABP25729	Drosophila melanog
706	6	1.2	159	21	AAU16353	Arabidopsis thalia	779	6	1.2	181	23	ABP25729	Arabidopsis thalia
707	6	1.2	159	21	AAU16353	Arabidopsis thalia	780	6	1.2	182	21	ABP25729	Novel human diagno
708	6	1.2	159	21	AAU16353	Arabidopsis thalia	781	6	1.2	182	22	ABP25729	Novel human diagno
709	6	1.2	159	21	AAU16353	Arabidopsis thalia	782	6	1.2	183	21	ABP25729	Arabidopsis thalia
710	6	1.2	159	21	AAU16353	Zea mays protein f	783	6	1.2	183	22	ABP25729	Drosophila melanog
711	6	1.2	159	21	AAU16353	Zea mays protein f	784	6	1.2	184	20	ABP25729	Chlamydia pneumoni
712	6	1.2	159	22	AAU29987	Streptococcus pneu	785	6	1.2	184	22	ABP25729	Zea mays protein f
713	6	1.2	159	22	AAU29987	Novel human secret	786	6	1.2	184	22	ABP25729	Propionibacterium
714	6	1.2	160	23	AAE20506	A. salmonicida typ	787	6	1.2	184	23	ABP25729	Human ATP-depend
715	6	1.2	160	23	AAE20506	Streptococcus muta	788	6	1.2	185	21	ABP25729	Arabidopsis thalia
716	6	1.2	161	20	AAU38038	Streptococcus muta	789	6	1.2	185	21	ABP25729	Arabidopsis thalia
717	6	1.2	161	20	AAU38038	Neisseria meningit	790	6	1.2	185	22	ABP25729	Drosophila melanog
718	6	1.2	161	21	AAU38038	Neisseria meningit	791	6	1.2	185	22	ABP25729	Propionibacterium
719	6	1.2	162	22	ABG11474	Zea mays protein f	792	6	1.2	185	22	ABP25729	Human gastric can
720	6	1.2	162	22	ABG11474	Novel human diagno	793	6	1.2	185	22	ABP25729	Human gastric can
721	6	1.2	162	22	ABG11474	Peptide #1604 enc	794	6	1.2	186	21	ABP25729	Z. mays COI1. Zea
722	6	1.2	162	22	ABG11474	Protein #8987 enco	795	6	1.2	186	21	ABP25729	Corn COI1 protein
723	6	1.2	162	22	ABG11474	Human expressed po	796	6	1.2	186	22	ABP25729	Human polypeptide
724	6	1.2	162	22	ABG11474	Human brain expres	797	6	1.2	186	22	ABP25729	Human novel foetal
725	6	1.2	162	22	ABG11474	Human bone marrow	798	6	1.2	187	22	ABP25729	Arabidopsis thalia
726	6	1.2	162	22	ABG11474	Human immune/haema	799	6	1.2	188	21	ABP25729	Arabidopsis thalia
727	6	1.2	162	22	ABG11474	Peptide #8164 enco	800	6	1.2	188	21	ABP25729	Arabidopsis thalia
728	6	1.2	162	22	ABG11474	Peptide #12083 enc	801	6	1.2	189	22	ABP25729	Arabidopsis thalia
729	6	1.2	162	22	ABG11474	Callitrix jacchus	802	6	1.2	189	22	ABP25729	Propionibacterium
730	6	1.2	163	22	ABG11474	Human peptide enco	803	6	1.2	189	22	ABP25729	Arabidopsis thalia
731	6	1.2	163	22	ABG11474	Dendritic cell (DC	804	6	1.2	190	21	ABP25729	Arabidopsis thalia
732	6	1.2	164	20	AAU27204	Amino acid sequenc	805	6	1.2	191	22	ABP25729	Novel human secret
733	6	1.2	164	21	AAU27204	Human secreted pro	806	6	1.2	191	22	ABP25729	Novel G protein co
734	6	1.2	164	21	AAU27204	Arabidopsis thalia	807	6	1.2	192	22	ABP25729	Drosophila melanog
735	6	1.2	164	21	AAU27204	Arabidopsis thalia	808	6	1.2	193	21	ABP25729	Arabidopsis thalia
736	6	1.2	164	21	AAU27204	Membrane-bound pro	809	6	1.2	193	22	ABP25729	Peptide #1608 enco
737	6	1.2	164	22	AAU66313	Propionibacterium	810	6	1.2	193	22	ABP25729	Peptide #1631 enco
738	6	1.2	164	22	AAU66313	S cerevisiae apopt	811	6	1.2	193	22	ABP25729	Protein #1565 enco
739	6	1.2	165	21	AAU66313	Zea mays protein f	812	6	1.2	193	22	ABP25729	Human brain expres
740	6	1.2	166	22	AAU66313	Novel human enzyme	813	6	1.2	193	22	ABP25729	Human bone marrow

522	1.2	105	22	AAG76799	Human colon cancer	595	1.2	122	22	AAUA3828	Propionibacterium
523	1.2	105	23	ABP35552	Human ORF4525 prot	596	1.2	122	22	ABG02444	Novel human diagno
524	1.2	105	23	ABP03375	Human ORFX protein	597	1.2	122	22	ABBI0328	Human cDNA SEQ ID
525	1.2	106	22	AAU64748	Propionibacterium	598	1.2	122	22	AAU18491	Human endocrine po
526	1.2	106	22	AAU63551	Human protein sequ	599	1.2	122	22	AAU79684	Human protein SEQ
527	1.2	107	10	AAU95449	Sequence encoded b	600	1.2	122	22	AAU43570	Human polypeptide
528	1.2	107	10	AAU39627	Propionibacterium	601	1.2	122	22	AAU80306	Human prostate can
529	1.2	108	21	AAG39333	Arabidopsis thalia	602	1.2	122	22	AAU19671	Human novel extrac
530	1.2	108	21	AAG74393	Human colon cancer	603	1.2	122	22	AAU21699	Novel human neopla
531	1.2	109	21	AAG36096	Zea mays protein f	604	1.2	122	22	ABF47891	Human polypeptide
532	1.2	109	22	AAU50864	Propionibacterium	605	1.2	122	23	ABG14065	Arabidopsis thalia
533	1.2	109	22	AAU53521	Propionibacterium	606	1.2	124	21	AAG14065	Arabidopsis thalia
534	1.2	109	22	ABU27651	Human peptide #302	607	1.2	124	22	AAU28122	Novel human secret
535	1.2	109	22	ABU32821	Peptide #327 encod	608	1.2	125	17	AAU91230	Rabbit G-protein c
536	1.2	109	22	ABU18303	Protein #302 encod	609	1.2	125	18	AAU09642	Rabbit G-protein-1
537	1.2	109	22	AAU82096	Human haematologic	610	1.2	125	23	ABF322725	Human ORF1698 prot
538	1.2	109	22	AAU53628	Human brain expres	611	1.2	126	16	AAU66984	African Green Monk
539	1.2	109	22	AAU66007	Human bone marrow	612	1.2	126	16	AAU86310	Ly-6 terminal CIP
540	1.2	109	22	AAU90994	Human immune/haema	613	1.2	126	20	AAU35871	Chlamydia pneumoni
541	1.2	109	22	AAU13876	Peptide #310 encod	614	1.2	126	21	AAU24462	Human secreted pro
542	1.2	109	22	AAU23852	zebra EST encoded	615	1.2	126	21	AAU06673	Arabidopsis thalia
543	1.2	109	22	AAU26283	Peptide #320 encod	616	1.2	126	21	AAU22776	Arabidopsis thalia
544	1.2	109	22	AAU01619	Peptide #301 encod	617	1.2	126	21	AAU42873	Arabidopsis thalia
545	1.2	109	23	AAU35655	Human peptide enco	618	1.2	126	22	AAU06040	Novel human diagno
546	1.2	110	20	AAU43035	Rice serine palmit	619	1.2	127	23	AAU17459	Mouse secreted pro
547	1.2	110	21	AAU03802	Human secreted pro	620	1.2	128	16	AAU66983	Baboon complement
548	1.2	110	21	AAU01823	Propionibacterium	621	1.2	128	16	AAU86309	Ly-6 terminal CIP
549	1.2	110	23	ABP04607	Human ORFX protein	622	1.2	128	21	AAU06672	Arabidopsis thalia
550	1.2	110	23	ABP08577	Human ORFX protei	623	1.2	129	22	AAU05805	Human polypeptide
551	1.2	111	18	AAU55458	H. pylori ORF 02ap	624	1.2	130	20	AAU36126	Extended human sec
552	1.2	111	20	AAU11884	Human 5' EST secre	625	1.2	130	21	AAU47101	Arabidopsis thalia
553	1.2	111	21	AAU52526	Helicobacter pylor	626	1.2	130	21	AAU59790	Arabidopsis thalia
554	1.2	112	21	AAU25216	Eucalyptus grandis	627	1.2	130	21	AAU02147	Human ORFX protein
555	1.2	112	21	AAU41998	Arabidopsis thalia	628	1.2	131	21	AAU47100	Arabidopsis thalia
556	1.2	112	21	AAU58214	Feline CD40 fragme	629	1.2	131	22	ABG16171	Novel human diagno
557	1.2	112	22	AAU60798	Propionibacterium	630	1.2	132	22	AAU63065	Propionibacterium
558	1.2	112	23	ABP42131	Human ovarian anti	631	1.2	132	22	AAU14163	Human novel protei
559	1.2	113	22								

376	6	1.2	68	21	AAG03055	Human secreted pro	449	6	1.2	88	22	AAU58101	Propionibacterium
377	6	1.2	68	23	ABP07466	Human ORFX protein	450	6	1.2	88	22	AAO13637	Human polypeptide
378	6	1.2	69	21	AAG39334	Arabidopsis thalia	451	6	1.2	88	22	AAW41971	Human polypeptide
379	6	1.2	69	22	AAU52601	Propionibacterium	452	6	1.2	88	23	ABE48668	Listeria monocytog
380	6	1.2	70	22	ABG02382	Novel human diagno	453	6	1.2	89	22	ABE48668	Human secreted pro
381	6	1.2	71	22	AAG22745	Zea mays protein f	454	6	1.2	89	23	ABG64731	Human albumin fusi
382	6	1.2	71	22	AAG33487	Arabidopsis thalia	455	6	1.2	89	23	AAU72918	Neisseria meningit
383	6	1.2	72	21	AAU51740	Propionibacterium	456	6	1.2	90	22	ABE70084	Drosophila melanog
384	6	1.2	72	22	AAU52434	Propionibacterium	457	6	1.2	90	22	ABG74248	Human colon cancer
385	6	1.2	72	22	AAU66096	Propionibacterium	458	6	1.2	91	22	ABE67733	Drosophila melanog
386	6	1.2	72	22	ABE41790	Peptide #9296 enco	459	6	1.2	91	22	ABG01525	Novel human diagno
387	6	1.2	72	22	ABE25518	Protein #7517 enco	460	6	1.2	91	22	ABG34158	C glutamicum prote
388	6	1.2	72	22	ABE26662	Human brain expres	461	6	1.2	92	21	AAG34719	Arabidopsis thalia
389	6	1.2	72	22	AAW75480	Human bone marrow	462	6	1.2	92	22	AAU00780	Arabidopsis thalia
390	6	1.2	72	22	AAU20600	Peptide #7034 enco	463	6	1.2	92	22	AAW77580	Udp-N-Acetylmuramo
391	6	1.2	72	22	AAW35586	Peptide #9623 enco	464	6	1.2	93	21	AAV65015	Human 5' EST relat
392	6	1.2	72	22	AAG75353	Human colon cancer	465	6	1.2	93	22	ABG10532	Novel human diagno
393	6	1.2	72	22	ABG45041	Human peptide enco	466	6	1.2	93	22	ABG15611	Novel human diagno
394	6	1.2	73	22	AAU62590	Propionibacterium	467	6	1.2	93	23	AAO06744	Human ovarian anti
395	6	1.2	73	22	AAU65472	Propionibacterium	468	6	1.2	93	23	ABP42440	Arabidopsis thalia
396	6	1.2	73	22	AAG92918	C glutamicum prote	469	6	1.2	94	22	ABE69031	Drosophila melanog
397	6	1.2	74	20	AAZ25741	Human secreted pro	470	6	1.2	94	22	ABG10742	Novel human diagno
398	6	1.2	74	23	ABP07579	Human ORFX protein	471	6	1.2	95	21	AAG32798	Zea mays protein f
399	6	1.2	75	20	AAU27314	Baboon CD59 protei	472	6	1.2	95	21	AAG59791	Arabidopsis thalia
400	6	1.2	75	22	ABG03850	Novel human diagno	473	6	1.2	95	22	AAU42795	Propionibacterium
401	6	1.2	75	22	ABG10360	Novel human diagno	474	6	1.2	95	22	AAU67212	Propionibacterium
402	6	1.2	75	22	ABG14248	Novel human diagno	475	6	1.2	95	22	ABG09699	Novel human diagno
403	6	1.2	75	22	ABG19650	Novel human diagno	476	6	1.2	95	23	AAW48987	Human glutamate re
404	6	1.2	76	20	AAU01435	Secreted protein e	477	6	1.2	96	21	AAG14994	Arabidopsis thalia
405	6	1.2	76	22	AAU39653	Propionibacterium	478	6	1.2	96	22	AAW84483	Human immune/haema
406	6	1.2	76	22	AAW90866	Human immune/haema	479	6	1.2	96	23	AAE19325	Vibrio cholerae ac
407	6	1.2	76	23	ABP00922	Human ORFX protein	480	6	1.2	96	23	ABE49014	Listeria monocytog
408	6	1.2	77	20	AAZ27315	African green monk	481	6	1.2	97	22	AAU53169	Propionibacterium
409	6	1.2	77	21	AAG27169	Zea mays protein f	482	6	1.2	97	22	ABG16475	Novel human diagno
410	6	1.2	77	21	AAG56886	Arabidopsis thalia	483	6	1.2	97	22	ABE10864	Human ovarian and/
411	6	1.2	77	23	ABP33911	Human ORF2884 prot	484	6	1.2	97	22	AAW94672	Human reproductive
412	6	1.2	77	23	ABP10551	Human ORFX protein	485	6	1.2	97	22	AAW91072	Human immune/haema
413	6	1.2	78	22	AAU67847	Propionibacterium	486	6	1.2	97	23	ABP41475	Human ovarian anti
414	6	1.2	79	21	AAG32799	Zea mays protein f	487	6	1.2	98	16	AAE69098	Tick-derived prote
415	6	1.2	79	22	ABG35664	Human colon cancer	488	6	1.2	98	16	AAE68039	Kunitz protease in
416	6	1.2	79	22	ABG59531	Human secreted pro	489	6	1.2	98	22	AAU16250	Human novel secret
417	6	1.2	79	23	ABP01626	Human ORFX protein	490	6	1.2	98	23	ABP03272	Human ORFX protein
418	6	1.2	80	16	AAW74997	E. maxima Em70-1 N	491	6	1.2	99	22	ABE29502	Peptide #2153 enco
419	6	1.2	80	22	AAU39966	Propionibacterium	492	6	1.2	99	22	ABE29502	Human brain expres
420	6	1.2	80	22	AAU40914	Propionibacterium	493	6	1.2	99	22	AAU55472	Human polypeptide
421	6	1.2	80	22	AAU46520	Propionibacterium	494	6	1.2	100	14	AAW44819	Sequence of the ga
422	6	1.2	80	22	AAU07160	Human secreted pro	495	6	1.2	100	21	AAG34718	Arabidopsis thalia
423	6	1.2	81	21	AAW91643	Human polypeptide	496	6	1.2	100	22	AAU44911	Propionibacterium
424	6	1.2	81	22	ABE65769	Drosophila melanog	497	6	1.2	100	22	ABG29057	Novel human diagno
425	6	1.2	81	22	AAU57229	Propionibacterium	498	6	1.2	100	22	ABP34755	Human ORF3728 prot
426	6	1.2	82	20	AAW11880	Human 5' EST secre	499	6	1.2	100	23	ABP00345	Human ORFX protein
427	6	1.2	82	20	AAW13165	Human secreted pro	500	6	1.2	100	23	ABP00345	NAD-dependent 2-hy
428	6	1.2	82	21	AAG00301	Human secreted pro	501	6	1.2	100	23	AAU77466	Arabidopsis thalia
429	6	1.2	82	21	AAW91557	Human secreted pro	502	6	1.2	101	21	AAG14993	Arabidopsis thalia
430	6	1.2	83	21	AAU59180	Arabidopsis thalia	503	6	1.2	101	22	AAU62689	Propionibacterium
431	6	1.2	83	22	AAU63954	Propionibacterium	504	6	1.2	101	22	AAG76383	Human colon cancer
432	6	1.2	83	22	AAU15954	Human novel secret	505	6	1.2	102	20	AAW37894	Amino acid sequenc
433	6	1.2	83	23	ABE97584	Novel human protei	506	6	1.2	102	21	AAG14992	Arabidopsis thalia
434	6	1.2	84	18	AAW53264	H. pylori ORF 06ge	507	6	1.2	102	22	ABE68971	Drosophila melanog
435	6	1.2	84	20	AAW13120	Human secreted pro	508	6	1.2	102	22	AAO07394	Human polypeptide
436	6	1.2	84	21	AAG35192	Zea mays protein f	509	6	1.2	103	22	AAO04892	Human polypeptide
437	6	1.2	85	21	AAG14831	Arabidopsis thalia	510	6	1.2	104	21	AAG12768	Arabidopsis thalia
438	6	1.2	85	22	ABE70952	Drosophila melanog	511	6	1.2	104	21	AAG11777	Zea mays protein f
439	6	1.2	85	22	AAU39202	Propionibacterium	512	6	1.2	104	22	AAU54662	Propionibacterium
440	6	1.2	86	22	AAW83140	Human immune/haema	513	6	1.2	104	22	AAW56567	Human brain expres
441	6	1.2	86	22	AAG75375	Human colon cancer	514	6	1.2	104	22	AAW90223	Human immune/haema
442	6	1.2	87	21	AAG04827	Arabidopsis thalia	515	6	1.2	104	22	AAW38534	Peptide #12571 enc
443	6	1.2	87	21	AAG19718	Arabidopsis thalia	516	6	1.2	104	23	ABG47300	Human peptide enco
444	6	1.2	87	21	AAG56885	Arabidopsis thalia	517	6	1.2	105	21	AAG12806	Arabidopsis thalia
445	6	1.2	87	21	AAG61015	Arabidopsis thalia	518	6	1.2	105	21	AAG16051	Arabidopsis thalia
446	6	1.2	87	23	ABE97911	Human secretory po	519	6	1.2	105	21	AAG17682	Arabidopsis thalia
447	6	1.2	88	21	ABG59792	Arabidopsis thalia	520	6	1.2	105	21	AAG34542	Arabidopsis thalia
448	6	1.2	88	22	AAU56714	Propionibacterium	521	6	1.2	105	22	AAU22401	Human cardiovascul

230	6	1.2	9	17	AAW06996	Synthetic peptide	303	6	1.2	48	21	AAV87940	Murine intracellular
231	6	1.2	9	17	AAW07003	Synthetic peptide	304	6	1.2	48	21	AAV87941	Hamster intracellular
232	6	1.2	9	22	AAU26674	Human Leukocyte An	305	6	1.2	49	20	AAV11838	Human 5' EST seque
233	6	1.2	9	22	AAU27007	Human Leukocyte An	306	6	1.2	50	20	AAU62442	Propionibacterium
234	6	1.2	10	22	AAU26709	Human Leukocyte An	307	6	1.2	51	22	AAU63623	Propionibacterium
235	6	1.2	10	22	AAU26710	Human Leukocyte An	308	6	1.2	51	22	ABB14755	Human nervous syst
236	6	1.2	10	22	AAU27042	Human Leukocyte An	309	6	1.2	52	20	AAV60419	Human normal bladd
237	6	1.2	10	22	AAU27043	Human Leukocyte An	310	6	1.2	52	20	AAU48265	Propionibacterium
238	6	1.2	10	22	AAG95487	Human complementar	311	6	1.2	52	22	AAU53365	Propionibacterium
239	6	1.2	10	22	AAG88080	Saccharomyces cere	312	6	1.2	52	22	AAU59620	Propionibacterium
240	6	1.2	10	22	AAG88081	Saccharomyces cere	313	6	1.2	53	21	AAU40807	Human ORFX ORF571
241	6	1.2	10	22	AAG88082	Saccharomyces cere	314	6	1.2	53	21	AAU41337	Propionibacterium
242	6	1.2	10	22	AAG88083	Saccharomyces cere	315	6	1.2	53	23	ABP31545	Human ORF518 prote
243	6	1.2	10	22	AAG88084	Saccharomyces cere	316	6	1.2	53	23	ABP35065	Human transport pr
244	6	1.2	10	22	AAG88085	Saccharomyces cere	317	6	1.2	54	22	AAU60212	Propionibacterium
245	6	1.2	12	23	AAU47714	Peptide B1.3. Syn	318	6	1.2	54	22	ABU44495	Peptide #12001 enc
246	6	1.2	12	23	AAU47714	Peptide B1.3. Syn	319	6	1.2	54	22	ABU44495	Protein #9320 enco
247	6	1.2	14	22	AAU97514	Human peptide #789	320	6	1.2	54	22	ABU03273	Human musculoskele
248	6	1.2	15	15	AAU47724	HIV epitope #57.	321	6	1.2	54	22	AAU22092	Peptide #8526 enco
249	6	1.2	15	15	AAU44382	Morphinone reducta	322	6	1.2	54	23	ABP00424	Human ORFX protein
250	6	1.2	15	23	AAU77467	NAD-dependent 2-hy	323	6	1.2	55	22	AAU48999	Propionibacterium
251	6	1.2	19	23	AAU10419	PARI pepducin plpa	324	6	1.2	56	22	AAU34269	Staphylococcus aur
252	6	1.2	21	22	AAU88704	Human interleukin-	325	6	1.2	56	22	AAU84578	Human immune/haema
253	6	1.2	22	22	AAU74407	H cadherin transme	326	6	1.2	57	23	ABP34138	Human ORF3111 prot
254	6	1.2	24	20	AAU13214	Human secreted pro	327	6	1.2	57	23	AAU58438	Propionibacterium
255	6	1.2	27	19	AAU49894	Amino acid sequenc	328	6	1.2	59	22	ABU11178	Peptide #8684 enco
256	6	1.2	27	21	AAU32369	Human ClqRp trypti	329	6	1.2	59	22	ABU11178	Protein #7203 enco
257	6	1.2	27	22	AAU82194	Human immune/haema	330	6	1.2	59	22	AAU62038	Human brain expres
258	6	1.2	28	20	AAU88878	Polypeptide fragme	331	6	1.2	59	22	AAU74840	Human bone marrow
259	6	1.2	28	22	ABU50944	Human secreted pro	332	6	1.2	59	22	AAU89001	Human immune/haema
260	6	1.2	28	22	AAU72850	Human bone marrow	333	6	1.2	59	22	AAU34957	Peptide #8994 enco
261	6	1.2	28	23	AAU33081	Peptide #7118 enco	334	6	1.2	59	22	AAU10111	Human ion channel-
262	6	1.2	28	23	ABU42680	Human peptide enco	335	6	1.2	59	23	ABU44621	Human peptide enco
263	6	1.2	30	17	AAU98027	Fusogenic peptide	336	6	1.2	59	23	ABU06783	Human ORFX protein
264	6	1.2	31	21	AAU51836	Human secreted pro	337	6	1.2	60	21	AAU02632	Human secreted pro
265	6	1.2	31	21	AAU44702	Human secreted pro	338	6	1.2	60	22	AAU42670	Propionibacterium
266	6	1.2	34	21	AAU32352	Human ClqRp peptid	339	6	1.2	60	22	ABU16474	Novel human diagno
267	6	1.2	34	22	ABU41223	Peptide #8729 enco	340	6	1.2	60	22	ABU16474	Peptide #1570 enco
268	6	1.2	34	22	ABU25229	Protein #7228 enco	341	6	1.2	60	22	ABU28919	Peptide #1598 enco
269	6	1.2	34	22	AAU21168	Human novel foetal	342	6	1.2	60	22	ABU34092	Human nervous syst
270	6	1.2	34	22	AAU62085	Human brain expres	343	6	1.2	60	22	ABU15095	Human nervous syst
271	6	1.2	34	22	AAU74887	Human bone marrow	344	6	1.2	60	22	ABU19529	Protein #1528 enco
272	6	1.2	34	22	AAU20445	Peptide #6879 enco	345	6	1.2	60	22	AAU94654	Human reproductive
273	6	1.2	34	22	AAU35003	Peptide #9040 enco	346	6	1.2	60	22	AAU54877	Human brain expres
274	6	1.2	34	23	ABU44654	Human peptide enco	347	6	1.2	60	22	AAU67258	Human bone marrow
275	6	1.2	38	22	AAU77581	Human colon cancer	348	6	1.2	60	22	AAU15102	Peptide #1536 enco
276	6	1.2	40	22	AAU67460	Peptide derived fr	349	6	1.2	60	22	AAU27551	Peptide #1588 enco
277	6	1.2	41	21	AAU24502	Human secreted pro	350	6	1.2	60	22	AAU02839	Peptide #1521 enco
278	6	1.2	43	23	ABU51038	Human secreted pro	351	6	1.2	60	23	ABU36909	Human peptide enco
279	6	1.2	44	20	AAU60437	Human colon specif	352	6	1.2	61	21	AAU14344	Human ORF58 protei
280	6	1.2	44	22	AAU37426	Human normal bladd	353	6	1.2	61	21	AAU02185	Bovine pancreatic
281	6	1.2	44	22	ABU27699	Staphylococcus aur	354	6	1.2	61	22	AAU48451	Human secreted pro
282	6	1.2	44	22	ABU2870	Human peptide #350	355	6	1.2	61	22	ABU34904	Propionibacterium
283	6	1.2	44	22	ABU33853	Peptide #376 enco	356	6	1.2	62	22	AAU40461	Propionibacterium
284	6	1.2	44	22	ABU18352	Peptide #11359 enc	357	6	1.2	62	22	AAU29741	Peptide #2392 enco
285	6	1.2	44	22	ABU26781	Protein #351 enco	358	6	1.2	62	22	ABU34912	Peptide #2418 enco
286	6	1.2	44	22	AAU53672	Human brain expres	359	6	1.2	62	22	ABU20326	Protein #2325 enco
287	6	1.2	44	22	AAU64829	Human brain expres	360	6	1.2	62	22	AAU55723	Human brain expres
288	6	1.2	44	22	AAU66056	Human bone marrow	361	6	1.2	62	22	AAU55723	Human bone marrow
289	6	1.2	44	22	AAU77579	Human bone marrow	362	6	1.2	62	22	AAU15925	Peptide #2359 enco
290	6	1.2	44	22	AAU13925	Peptide #359 enco	363	6	1.2	62	22	AAU15925	Peptide #2465 enco
291	6	1.2	44	22	AAU21509	Peptide #7943 enco	364	6	1.2	62	22	AAU28428	Peptide #2343 enco
292	6	1.2	44	22	AAU26331	Peptide #368 enco	365	6	1.2	62	22	AAU36661	Human peptide enco
293	6	1.2	44	22	AAU37763	Peptide #11800 enc	366	6	1.2	62	22	AAU36661	Human peptide enco
294	6	1.2	44	22	AAU01668	Peptide #350 enco	367	6	1.2	63	21	AAG36050	Zeae mays protein f
295	6	1.2	44	23	ABU35704	Human peptide enco	368	6	1.2	63	21	AAG60726	Human secreted pro
296	6	1.2	44	23	ABU46610	Human peptide enco	369	6	1.2	65	22	AAU56632	Human secreted pro
297	6	1.2	45	9	AAU81952	Probable C-termina	370	6	1.2	65	22	AAU56632	Propionibacterium
298	6	1.2	45	20	AAU45284	Human secreted pro	371	6	1.2	65	23	ABU05332	C glutamicum prote
299	6	1.2	47	21	AAU64794	Human 5' EST relat	372	6	1.2	66	23	ABU35526	Human ORFX protein
300	6	1.2	48	19	AAU21219	Human bcl2 proto-o	373	6	1.2	66	22	AAU54088	Propionibacterium
301	6	1.2	48	21	AAU04829	Arabidopsis thalia	374	6	1.2	67	22	AAU59543	Propionibacterium
302	6	1.2	48	21	AAU87939	Rat intracellular	375	6	1.2	68	20	AAU13085	Human secreted pro

84	7	1.4	282	22	AAU61956	Propionibacterium	157	7	1.4	535	14	AAU42201	Diphtheria toxin (
85	7	1.4	293	22	AAU31016	Novel human secret	158	7	1.4	535	15	AAU44888	Wild-type diphther
86	7	1.4	299	22	AAU87532	Novel central nerv	159	7	1.4	535	17	AAU86825	Diphtheria toxin-
87	7	1.4	299	22	AAU19738	Human novel extrac	160	7	1.4	535	17	AAU86826	Diphtheria toxin (
88	7	1.4	299	23	ABP47958	Human polypeptide	161	7	1.4	535	18	AAU46448	Amino acid sequenc
89	7	1.4	307	20	AAU38843	Neisseria meningit	162	7	1.4	535	18	AAU24876	Diphtheria toxin.
90	7	1.4	313	21	AAU91033	Breast and ovarian	163	7	1.4	535	19	AAU68090	Diphtheria toxin c
91	7	1.4	317	23	ABU91087	Herbicidally activ	164	7	1.4	535	21	AAU97280	Wild type diphther
92	7	1.4	331	20	AAU67889	Human secreted pro	165	7	1.4	535	21	AAU96456	Diphtheria toxin (
93	7	1.4	332	21	AAU60684	Arabidopsis thalia	166	7	1.4	547	21	AAU96854	A. thaliana AS11 m
94	7	1.4	334	21	AAU60683	Arabidopsis thalia	167	7	1.4	560	7	AAU60516	Tox228 diphtheria t
95	7	1.4	336	21	AAU60682	Arabidopsis thalia	168	7	1.4	560	8	AAU0597	Modified diphtheri
96	7	1.4	340	22	ABU70792	Drosophila melanog	169	7	1.4	560	11	AAU06815	Gly(158) Diphtheri
97	7	1.4	341	23	ABU41484	Human ovarian anti	170	7	1.4	567	11	AAU06607	Porcine chondrocyt
98	7	1.4	388	19	AAU98375	H. pylori GHPO 113	171	7	1.4	599	21	AAU49966	Drosophila melanog
99	7	1.4	388	22	AAU35865	Helicobacter pylor	172	7	1.4	614	22	ABU70487	Hybrid protein DAB
100	7	1.4	388	22	AAU36030	Helicobacter pylor	173	7	1.4	619	23	AAU26486	Diphtheria toxin/U
101	7	1.4	401	18	AAU16339	DAB389-SP-Gly fusi	174	7	1.4	637	23	AAU75365	Diphtheria toxin/U
102	7	1.4	401	22	AAU95262	Human protein sequ	175	7	1.4	638	23	AAU75370	Diphtheria toxin-1
103	7	1.4	417	19	AAU54355	47 kD heat shock p	176	7	1.4	641	20	AAU99383	Diphtheria toxin-1
104	7	1.4	417	21	AAU81908	Human Hsp47 protei	177	7	1.4	642	23	AAU75382	Diphtheria toxin/U
105	7	1.4	418	23	AAU75577	Human heat shock p	178	7	1.4	643	23	AAU75390	Diphtheria toxin/U
106	7	1.4	419	21	AAU56928	Human prostate can	179	7	1.4	650	21	AAU31502	Arabidopsis thalia
107	7	1.4	420	22	AAU63605	Propionibacterium	180	7	1.4	652	21	AAU31501	Arabidopsis thalia
108	7	1.4	423	22	AAU69816	C glutamicum prote	181	7	1.4	652	23	AAU75448	Immunotoxin fusion
109	7	1.4	432	21	AAU43633	Amino acid sequenc	182	7	1.4	656	23	AAU75383	Immunotoxin fusion
110	7	1.4	449	21	AAU91341	Group B Streptococ	183	7	1.4	657	23	AAU75389	Diphtheria toxin/U
111	7	1.4	449	22	AAU03611	Group B Streptococ	184	7	1.4	671	19	AAU68500	Hybrid receptor to
112	7	1.4	449	23	ABP41485	Human ovarian anti	185	7	1.4	676	10	AAU93172	Quarter-length hyb
113	7	1.4	449	23	ABP26349	Streptococcus poly	186	7	1.4	676	21	AAU90706	Quarter-length hyb
114	7	1.4	452	19	AAU80217	48 kD modified di	187	7	1.4	676	22	AAU07526	Diphtheria toxin/B
115	7	1.4	453	21	AAU31504	Arabidopsis thalia	188	7	1.4	693	16	AAU66738	Cytochrome-P450-ox
116	7	1.4	454	22	ABU59773	Drosophila melanog	189	7	1.4	724	22	AAU87349	Novel central nerv
117	7	1.4	455	18	AAU34055	Modified Diphtheri	190	7	1.4	751	21	AAU31500	Arabidopsis thalia
118	7	1.4	463	22	AAU84086	Human protein sequ	191	7	1.4	756	22	AAU87329	Novel central nerv
119	7	1.4	463	23	AAU91382	Human secreted pro	192	7	1.4	794	18	AAU25637	Human cadherin-12
120	7	1.4	468	10	AAU90626	51 kD modified dip	193	7	1.4	794	18	AAU31335	Putative human cad
121	7	1.4	469	18	AAU34056	Modified Diphtheri	194	7	1.4	805	22	ABU59621	Drosophila melanog
122	7	1.4	470	23	ABP41784	Human ovarian anti	195	7	1.4	814	22	AAU34565	Human polypeptide
123	7	1.4	471	18	AAU26311	Human STCH chapero	196	7	1.4	820	22	AAU87115	Novel central nerv
124	7	1.4	472	18	AAU26312	Rat STCH chaperone	197	7	1.4	849	22	ABU05943	Novel human diagno
125	7	1.4	473	12	AAU14195	Rat cannabinoide re	198	7	1.4	869	10	AAU93171	Half-length hybrid
126	7	1.4	473	23	ABU57048	Mouse ischaemic co	199	7	1.4	869	21	AAU90705	Half-length hybrid
127	7	1.4	480	19	AAU80218	51 kDa modified di	200	7	1.4	869	22	AAU07525	Diphtheria toxin/B
128	7	1.4	506	20	AAU38844	Neisseria meningit	201	7	1.4	885	22	AAU32393	Novel human secret
129	7	1.4	506	20	AAU38845	Neisseria meningit	202	7	1.4	895	23	AAU75368	Diphtheria toxin/U
130	7	1.4	506	20	AAU38846	Neisseria gonorrhoe	203	7	1.4	895	23	AAU75369	Diphtheria toxin/U
131	7	1.4	518	14	AAU40208	Sequence of geneti	204	7	1.4	895	23	AAU75374	Diphtheria toxin/U
132	7	1.4	520	21	AAU19740	Arabidopsis acyl C	205	7	1.4	896	23	AAU75366	Diphtheria toxin/U
133	7	1.4	520	21	AAU94512	Arabidopsis diacyl	206	7	1.4	896	23	AAU75367	Diphtheria toxin/U
134	7	1.4	520	21	AAU94524	A. thaliana diacyl	207	7	1.4	896	23	AAU75373	Diphtheria toxin/U
135	7	1.4	520	21	AAU96853	A. thaliana diacyl	208	7	1.4	899	23	AAU75375	Diphtheria toxin/U
136	7	1.4	520	21	AAU54143	Acyl-CoA:cholester	209	7	1.4	920	22	ABU65710	Drosophila melanog
137	7	1.4	520	22	AAU00462	Arabidopsis thalia	210	7	1.4	1013	22	AAU32392	Novel human secret
138	7	1.4	524	21	AAU31503	Arabidopsis thalia	211	7	1.4	1184	20	AAU74445	Human nucleotide p
139	7	1.4	528	15	AAU44892	Diphtheria toxin (212	7	1.4	1184	21	AAU66657	Membrane-bound pro
140	7	1.4	528	22	ABU69018	Drosophila melanog	213	7	1.4	1184	22	AAU12377	Human PRO1188 poly
141	7	1.4	532	15	AAU44890	Diphtheria toxin d	214	7	1.4	1184	22	AAU65180	Human PRO1188 (UNQ
142	7	1.4	533	15	AAU44889	Diphtheria toxin d	215	7	1.4	1241	22	AAU25606	Human protein sequ
143	7	1.4	533	15	AAU44891	Diphtheria toxin (216	7	1.4	1293	22	AAU80214	Human protein sequ
144	7	1.4	533	15	AAU44893	Diphtheria toxin (217	7	1.4	1293	22	AAU80215	Human protein sequ
145	7	1.4	533	15	AAU44894	Diphtheria toxin (218	7	1.4	1323	22	AAU79231	Human protein sequ
146	7	1.4	533	15	AAU44895	Diphtheria toxin (219	7	1.4	1323	23	AAU66142	Human PAS Kinase (
147	7	1.4	533	15	AAU44896	Diphtheria toxin (220	7	1.4	1330	22	AAU79230	Human protein sequ
148	7	1.4	533	15	AAU44897	Diphtheria toxin (221	7	1.4	1330	22	AAU65630	Novel protein kina
149	7	1.4	533	15	AAU44898	Diphtheria toxin (222	7	1.4	1421	21	AAU58573	Sorangium celluloso
150	7	1.4	533	15	AAU44899	Diphtheria toxin (223	7	1.4	1698	22	ABU67538	Drosophila melanog
151	7	1.4	533	15	AAU44900	Diphtheria toxin (224	7	1.4	1828	17	AAU81531	BRCA1 mutant from
152	7	1.4	533	15	AAU44901	Diphtheria toxin (225	7	1.4	2391	15	AAU55694	Carbamoyl-phosphat
153	7	1.4	533	15	AAU44902	Diphtheria toxin (226	6	1.2	8	22	AAU69062	Bacterial conserve
154	7	1.4	534	19	AAU80216	Native Diphtheria	227	6	1.2	9	17	AAU49633	Human leucocyte an
155	7	1.4	535	10	AAU90181	Cross-reactive mat	228	6	1.2	9	17	AAU07037	Synthetic peptide
156	7	1.4	535	14	AAU40103	Diphtheria toxin f	229	6	1.2	9	17	AAU07006	Synthetic peptide

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16: /SIDS2/gcgdata/geneseq/geneseqp-s
17: /SIDS2/gcgdata/geneseq/geneseqp-t
18: /SIDS2/gcgdata/geneseq/geneseqp-u
19: /SIDS2/gcgdata/geneseq/geneseqp-v
20: /SIDS2/gcgdata/geneseq/geneseqp-w
21: /SIDS2/gcgdata/geneseq/geneseqp-x
22: /SIDS2/gcgdata/geneseq/geneseqp-y
23: /SIDS2/gcgdata/geneseq/geneseqp-z

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	100.0	500	23	Human Tumour Endot
2	500	100.0	1002	23	Human Tumour Endot
3	371	74.2	400	21	Human ORFX ORF2895
4	271	54.2	431	22	Human endotheial
5	130	26.0	146	23	Human polypeptide
6	108	21.6	205	22	Human immune/haema
7	68	13.6	108	19	Homo sapiens adult
8	68	13.6	108	22	Human CC194.4 prot
9	53	10.6	53	22	Peptide #6597 enco
10	53	10.6	53	22	Human brain expres

11	53	10.6	53	22	Human bone marrow
12	53	10.6	53	22	Peptide #6621 enco
13	53	10.6	53	22	Human peptidase enco
14	41	8.2	306	22	Novel human diago
15	35	7.0	500	23	Mouse Tumour Endot
16	35	7.0	500	23	Mouse Tumour Endot
17	13	2.6	1230	22	Novel human diago
18	11	2.2	140	23	Human ORFX protein
19	10	2.0	200	21	Human ORFX ORF263
20	10	2.0	392	22	Stem cell growth f
21	10	2.0	392	22	Stem cell growth f
22	10	2.0	425	22	Human polypeptide
23	10	2.0	425	22	Human polypeptide
24	10	2.0	427	22	Human polypeptide
25	10	2.0	427	22	Human polypeptide
26	10	2.0	449	22	Human polypeptide
27	10	2.0	486	22	Human polypeptide
28	10	2.0	499	22	Human polypeptide
29	10	2.0	529	22	Human PRO polypept
30	10	2.0	529	22	Human polypeptide
31	10	2.0	529	22	Stem cell growth f
32	10	2.0	529	22	Stem cell growth f
33	10	2.0	529	22	Human acid sequenc
34	10	2.0	529	23	Human Tumour Endot
35	10	2.0	530	23	Mouse Tumour Endot
36	10	2.0	530	23	Mouse Tumour Endot
37	8	1.6	68	23	Human ORFX protein
38	8	1.6	107	23	Human ORFX protein
39	8	1.6	169	22	Escherichia coli p
40	8	1.6	460	23	Streptococcus poly
41	8	1.6	625	22	Drosophila melanog
42	8	1.6	924	22	Novel human diago
43	7	1.4	11	20	Cyclosporin A muta
44	7	1.4	58	22	Propionibacterium
45	7	1.4	73	21	Arabidopsis thalia
46	7	1.4	74	19	Human secreted pro
47	7	1.4	75	22	Human papillomavir
48	7	1.4	77	22	Peptide #11396 enc
49	7	1.4	77	22	Human brain expres
50	7	1.4	80	23	Human ORFX protein
51	7	1.4	89	23	Human ORFX protein
52	7	1.4	96	20	pGR2P3 protein se
53	7	1.4	99	22	Human secreted pro
54	7	1.4	99	22	Human albumin fusi
55	7	1.4	110	21	Human secreted pro
56	7	1.4	110	21	Human secreted pro
57	7	1.4	110	22	Human secreted pro
58	7	1.4	110	23	Human secreted pro
59	7	1.4	112	22	Human albumin fusi
60	7	1.4	112	22	Human EST encoded
61	7	1.4	116	17	Human cannabinoi
62	7	1.4	119	21	Human ORFX ORF2912
63	7	1.4	120	20	Human protein sequ
64	7	1.4	129	22	Human protein sequ
65	7	1.4	131	22	Drosophila melanog
66	7	1.4	136	22	Avian infectious b
67	7	1.4	151	22	E. canis protein a
68	7	1.4	157	22	Propionibacterium
69	7	1.4	157	22	Drosophila melanog
70	7	1.4	178	22	Novel human diago
71	7	1.4	193	18	C glutamic prote
72	7	1.4	213	21	Human protein sequ
73	7	1.4	213	21	Human ORFX ORF2912
74	7	1.4	213	22	Human protein sequ
75	7	1.4	217	22	Drosophila melanog
76	7	1.4	225	19	Avian infectious b
77	7	1.4	225	22	E. canis protein a
78	7	1.4	229	22	Propionibacterium
79	7	1.4	260	22	Drosophila melanog
80	7	1.4	267	22	Novel human diago
81	7	1.4	270	22	C glutamic prote
82	7	1.4	274	22	Human protein sequ
83	7	1.4	274	22	Human colon cancer

FT Peptide 1...100
 XX /note= "predicted signal/leader peptide"
 PN W09814576-A2.
 XX
 PD 09-APR-1998.
 XX
 PF 03-OCT-1997; 97WO-US18007.
 XX
 PR 04-OCT-1996; 96US-0726237.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
 PI Racie LA, Spaulding V, Treacy M;
 XX WPI; 1998-240082/21.
 DR N-PSDB; AAV11619.
 XX
 XX Nucleic acids encoding novel secreted proteins - useful as, e.g.
 PT anti-inflammatory, immuno-stimulatory or suppressing agents
 PT
 XX Disclosure; Page 79; 110pp; English.
 PS
 CC The sequence is that of a secreted protein encoded by
 CC an isolated polynucleotide which may be of use in the
 CC production of therapeutic compositions for treating or
 CC ameliorating a medical condition in a mammal. Such compositions
 CC may be used for, e.g. research purposes as markers for
 CC tissues, molecular weight markers for gels, primers or probes, for
 CC nutrition as carbon, nitrogen or carbohydrate source. They can also be
 CC used as a cytokine for cell proliferation and differentiation activity,
 CC as immune stimulants or suppressors, e.g. for viral, bacterial or fungal
 CC infections, for autoimmune diseases such as multiple sclerosis or
 CC systemic lupus erythematosus, to regulate haematopoiesis, for tissue
 CC growth, as an activator or inhibitor, or as a chemotactic or
 CC chemokinetic, haemostatic and thrombocytic, receptor/ligand,
 CC anti-inflammatory or tumour inhibitor agents.
 XX
 SQ Sequence 108 AA;
 Query Match 13.6%; Score 68; DB 19; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.3e-60;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 383 TSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGPIVGIVLAVLLVAAIL 442
 DB 41 TSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGPIVGIVLAVLLVAAIL 100
 QY 443 AGIYINGH 450
 DB 101 AGIYINGH 108
 RESULT 8
 AAB90677
 ID AAB90677 standard; Protein; 108 AA.
 XX
 AC AAB90677;
 XX
 DT 07-JUN-2001 (first entry)
 XX
 DE Human CC194_4 protein sequence SEQ ID 30.
 XX
 KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KW differentiation; immune system modulator; tissue growth; chemotactic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
 KW haematopoiesis.
 XX
 OS Homo sapiens.
 XX
 PN W0200119988-A1.
 XX

PD 22-MAR-2001.
 XX
 PF 14-SEP-2000; 2000WO-US25135.
 XX
 PR 17-SEP-1999; 99US-0398829.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
 XX WPI; 2001-244801/25.
 DR N-PSDB; AAF98392.
 XX
 XX Isolated nucleic acids encoding polypeptides, useful for modulating
 PT e.g. cytokine and cell proliferation/differentiation activity, the
 PT immune system and hematopoiesis regulating activity -
 XX
 PS Disclosure; Page 399; 557pp; English.
 XX
 CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic
 CC activity; receptor/ligand activity; anti-inflammatory activity;
 CC haematopoiesis activity; cadherin/tumour suppressor activity; and/or
 CC tumour inhibition activity. Included in the invention are probes
 CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones
 CC encoding the secreted proteins.
 XX
 SQ Sequence 108 AA;
 Query Match 13.6%; Score 68; DB 22; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.3e-60;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 383 TSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGPIVGIVLAVLLVAAIL 442
 DB 41 TSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGTPVHLGPIVGIVLAVLLVAAIL 100
 QY 443 AGIYINGH 450
 DB 101 AGIYINGH 108
 RESULT 9
 ABB39091
 ID ABB39091 standard; Peptide; 53 AA.
 XX
 AC ABB39091;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #6597 encoded by human foetal liver single exon probe.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 PN W0200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00669.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.

Query Match 10.6%; Score 53; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 2.8e-45;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 HDEGPGSGWAAGTIVGNNRRARESPGHVSEPDRTQLSDLGSGGTFLAMDTLPD 79
 DB 1 HDEGPGSGWAAGTIVGNNRRARESPGHVSEPDRTQLSDLGSGGTFLAMDTLPD 53

RESULT 12
 AAM32584
 ID AAM32584 standard; Protein; 53 AA.
 AC AAM32584;
 XX
 XX
 DT 17-OCT-2001 (first entry)
 DE Peptide #6621 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00663.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 XX
 PS Claim 27; SEQ ID No 32853; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENPs;
 CC see AA13315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 XX
 SQ Sequence 53 AA;

Query Match 10.6%; Score 53; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 2.8e-45;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 HDEGPGSGWAAGTIVGNNRRARESPGHVSEPDRTQLSDLGSGGTFLAMDTLPD 79
 DB 1 HDEGPGSGWAAGTIVGNNRRARESPGHVSEPDRTQLSDLGSGGTFLAMDTLPD 53

RESULT 13
 ABG42140
 ID ABG42140 standard; Peptide; 53 AA.
 XX
 AC ABG42140;

XX
 DT 19-AUG-2002 (first entry)
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 31805.
 DE
 DE
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00665.
 XX
 PR 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 DR
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 XX
 PS Claim 27; SEQ ID No 31805; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridize at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridization of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary

haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karageners syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://www.wipo.int/pub/published/pct_sequences.

Seq	Sequence	53 AA;	Query Match	10.6%;	Score 53;	DB 23;	Length 53;		
			Best Local Similarity	100.0%;	Pred. No. 2.8e-45;				
			Matches 53;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	27	HDEGPGSGWAAKGTVRGWNRRARESPGVHSEFPDRTQLSODLGGGTLMAMDTLPD	79						
Db	1	HDEGPGSGWAAKGTVRGWNRRARESPGVHSEFPDRTQLSODLGGGTLMAMDTLPD	53						

RESULT 14
ABG09319
ID ABG09319 standard: Protein: 306 AA:

XX AC ABG09319:

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #9310.

Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW

AA . Homo sapiens. OS

PN WO200175067-A2.

PD 11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000: 2000US-0540217.

PR 23-AUG-2000; 2000US-0849187:
XX

PA (HYSE-) HYSEQ INC.
VY

PI Drmanac RT, Liu C, Tang YI;

DR WPI; 2001-639362/73.

XX
XX

PT diagnostics, forensics, gene mapping, identification of mutations
PT· responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 20; SEQ ID No 39678; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at www.wipo.int/pub/published/pct_sequences.

Sequence	306 AA;
----------	---------

Query Match	8.2%;	Score 41;	DB 22;	Length 306;
Best Local Similarity	100.0%;	Pred. No. 1.8e-32;		

41, conservative 0, atomized 0, mixed 0, self-

QY 138 F1FMGDV1HRMELIATQIVAPLEMANFNFGISDNSTVITDNG 138

4 / FIFMGDV IHRMLTATQI VAP LMANFNGISDNSIVVIEDNG 37

RESULT 15

ABB90729
ID ABB90729 standard: Protein: 500 AA.

XX
XC
APDQ0720.

XX
DT
30-MAY-70XX
Meiosis Endothelial M[illegible]

KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis.

OS Mus musculus.

AA WO200210217-A2.
PN

07-FEB-2002.

01-AUG-2001: 2001WO-US24031.

XX
PR 02-AUG-2000: 2000US-222599P-

PR 11-AUG-2000; 2000US-224360F.
PR 11-APR-2001; 2001US-282850P

XX
XX
FIVE TO A FIFTY TONS HOPKINS

[illegible]XX
 000 001050/000

XX An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth -
PT

PS Disclosure: Page 146-147; 331pp; English.

The invention relates to an isolated molecule comprising an antibody
 variable region which specifically binds to an extracellular domain of a
 tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 proteins have cytostatic, immunostimulant and antiangiogenic activity.
 They are useful for inhibiting tumour growth, neoangiogenesis in
 subjects bearing a vascularised tumour, polycystic kidney disease,
 diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 and pan-endothelial markers (PEM) ABL91903-ABL91995.

XX
XX

SQ Sequence 500 AA;

Query Match 7.0%; Score 35; DB 23; Length 500;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 HRQASRVVLSFDFFPYGHPLRQITTIATGGFIFMGD 163
 ||||||||||||||||||||||||||||||||||
 Db 130 HRQASRVVLSFDFFPYGHPLRQITTIATGGFIFMGD 164

Search completed: April 22, 2003, 16:16:53
 Job time : 67 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:05:15 ; Search time 16 seconds
(without alignments)
919.466 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELWLLVLVREARALS.....YAEVPSGHEKEGMEAEQC 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115.5	4.3	1568	4	US-09-181-706-2
2	115.5	4.3	1568	4	US-09-458-791-2
3	115.5	4.3	1568	4	US-09-459-066-2
4	95.5	3.5	3052	2	US-08-557-122A-26
5	95.5	3.5	3052	4	US-09-262-666-26
6	93	3.5	1085	1	US-08-431-080-28
7	93	3.5	1085	2	US-08-938-534-28
8	93	3.5	1085	4	US-09-345-294-28
9	92.5	3.4	1220	1	US-08-158-232-43
10	92.5	3.4	1220	2	US-08-611-928-43
11	92.5	3.4	1220	3	US-09-173-891-43
12	90.5	3.4	424	2	US-08-484-993B-18
13	90.5	3.4	424	2	US-08-484-158B-18
14	90.5	3.4	424	2	US-08-484-596A-18
15	90.5	3.4	424	2	US-08-480-150A-18
16	90.5	3.4	424	3	US-08-458-731-18
17	90.5	3.4	424	3	US-08-149-223A-18
18	89.5	3.3	424	6	5169835-6
19	89	3.3	595	2	US-08-232-087A-2
20	89	3.3	595	4	US-09-006-353A-9
21	89	3.3	595	4	US-09-573-986-9
22	88.5	3.3	15281	2	US-08-471-119A-2
23	88	3.3	595	1	US-08-225-989-2
24	88	3.3	595	1	US-08-570-923-2
25	88	3.3	595	1	US-08-580-014-2
26	88	3.3	595	4	US-09-079-785-2
27	88	3.3	606	4	US-09-041-236-4

28 87.5 3.3 659 4 US-09-562-737-13 Sequence 13, Appl
29 87.5 3.3 1969 3 US-08-836-325-16 Sequence 16, Appl
30 87.5 3.3 2133 4 US-09-523-656-30 Sequence 30, Appl
31 86.5 3.2 739 1 US-07-618-946B-22 Sequence 22, Appl
32 86.5 3.2 814 1 US-07-618-946B-23 Sequence 23, Appl
33 86 3.2 398 1 US-08-091-519-2 Sequence 2, Appl
34 86 3.2 398 1 US-08-442-043A-2 Sequence 2, Appl
35 86 3.2 398 4 US-09-173-151A-26 Sequence 2, Appl
36 86 3.2 398 5 PCT-US91-03478-2 Sequence 2, Appl
37 85.5 3.2 284 2 US-08-424-641B-2 Sequence 2, Appl
38 85.5 3.2 284 2 US-08-820-980-2 Sequence 2, Appl
39 85.5 3.2 284 2 US-08-826-439-2 Sequence 2, Appl
40 85.5 3.2 349 4 US-09-161-241-8 Sequence 8, Appl
41 85.5 3.2 834 3 US-08-539-205A-6 Sequence 6, Appl
42 84.5 3.1 1984 3 US-08-836-325-10 Sequence 10, Appl
43 84.5 3.1 1989 3 US-08-836-325-12 Sequence 12, Appl
44 84 3.1 572 6 5256770-7 Patent No. 5256770
45 84 3.1 575 1 US-08-312-870-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-181-706-2
; Sequence 2, Application US/09181706
; Patent No. 6130068

GENERAL INFORMATION:

APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. DuBoise, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09181,706
FILING DATE: October 28, 1998
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/958,598 (converted to a
APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631-A
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-181-706-2

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-459-066-2

Query Match 4.3%; Score 115.5; DB 4; Length 1568;
Best Local Similarity 20.6%; Pred. No. 0.047;
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

QY 39 CTVGRNRRARESPGHVSEPDRT-----QLSODLGGGTILAMDTLPDNRTRVVEDNHSYVVS 94
Db 256 GAATGWPSMAR-----IAQSTEVLFGQASLDCGHG-----PDGR-----R 292
QY 95 RLYGSEPHSRELWVAV--AEANRSQVKIHT-----LSNTHRAQSRVVLSE----- 139
Db 293 LLLSSSLVEALDVWAGVFAAGEGQERRSPTTALCLFRMSEIQARAKRVSWDFKTAES 352
QY 140 -----DEPEYGHPLRLQITATGGIFMGDVHRLMTATQYVAPLMAFNPCYSDNSTVYV 194
Db 353 HCKEGDQERVPQIASSTL-----IHSDLTSV-YGVVVM-----NRTVLF 391
QY 195 FDNQTFVYVQWHDVYVLOGWEDKGSFTFOAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249
Db 392 LGTG-----DGQLLKVLIGENLTSNCPVIEYKEE 422
QY 250 HPVKTGLSDAPMLNPSDPVPSRRRSIFEVHRIELDPKVTMSAVEFTPLPTCLOHRS 309
Db 423 TPV-----FYKLVPDP-----VKNIIYI-----LTAGKEVRRIRVANCNKHKS.460
QY 310 CDACMSSDLTFCNSCHVLCORCSSGFORYOE-----NWDYCAQAEAGRCWCEDEQ-----D 361
Db 461 CSECTA--TDPHCWGLSLQKCTFGQDCVHSENLENMLDI-----SSGAKKCPKIQTIRSS 515
QY 362 EDHDSASPTSFSP 375
Db 516 KEKTTVTWVGSFSP 529

RESULT 4
US-08-557-122A-26
; Sequence 26, Application US/08557122A
; Patent No. 5879664
; GENERAL INFORMATION:
; APPLICANT: Hjort, Carsten Molland
; TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5879664o No. 5879664disk of No. 5879664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,122A
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3980.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 3052 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-557-122A-26

Query Match 3.5%; Score 95.5; DB 2; Length 3052;
Best Local Similarity 18.5%; Pred. No. 13;
Matches 88; Conservative 52; Mismatches 190; Indels 145; Gaps 17;

QY 80 NRTVRVEDNHSYVYRLYGSEPHSREL---WVDVAEANRSQVKIHTILSNTHRQA----- 132
Db 2396 NFEVAFDEKKNVFEFYAPWCCHCKOLAPWIDKLGELYKEHODI-VIAKNEFEVAFDEN 2454
QY 133 SRVLSFDFEYFGHPLRQITATGGIFMGDVHRLMTATQYVAPLMAFNPCYSDNSTV 192
Db 2455 KNVFEFYAPWCCH-----CKQLAPAWDKLGPYRDEHNI 2489
QY 193 VYFDNGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRIVFAYKEI-----PMSVP 243
Db 2490 VIAKN-----HDEIVNDPKDVLVLYAPWCCHCKRLAPTQELADTYANATSDVLA 2542
QY 244 EISSQHPVKTGLSDAPMLNPSDPVPSRRRSIFEYH-----RI 283
Db 2543 KMDSTANEVAVKVSFPPTLK---FFPASADRTVIDYNGERTLDGPKFKFLESGGMDSTAN 2599
QY 284 ELDPKSVTMSAVEFTPLPTCLQHRSCDACMSSDLT---FNCSWCHVLCORCSSGFORYO 340
Db 2600 EVEAVKVSFPPTLKFPF-----ASADRTVIDYNG-----BRTLDGFKKFL 2640
QY 341 EMWDYCAQAEAGRCWCEDEQDEHDSASPTSFSPYDGLTTTSSSLFIDSITTEDDTKL 400
Db 2641 SGGMDSTANEVAVKVSFPPTLKFPFASADRTVIDYNGERTLDGFKKFL 2691
QY 401 NPYAGGDLQNNLS-----PKTKGTPVHLGTIVGIVLAVLLVAILLAGIYINGHPTS 453
Db 2692 ---GGMDSTANEVAVKVSFPPTLKFPFAGPGRTV-----IDYNGERTL 2732
QY 454 NAALFFIER-----RPHHPAMKFRSHPDHSTYAEVPSGHEK-EGF 494
Db 2733 DGFKFKFLESGGMDSTANEVAVKVSFPPTLKFPFAGSGRNVIDYNGERTLEGF 2785

RESULT 5
US-09-262-666-26
; Sequence 26, Application US/09262666
; Patent No. 6346244
; GENERAL INFORMATION:
; APPLICANT: Hjort, Carsten Molland
; TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6346244o No. 6346244disk of No. 6346244th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/262,666
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,122
; FILING DATE: 11-DEC-1995
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3980.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3052 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-262-666-26

Query Match 3.5%; Score 95.5; DB 4; Length 3052;
Best Local Similarity 18.5%; Pred. No. 13; Mismatches 190; Indels 145; Gaps 17;
Matches 88; Conservative 52;

QY 80 NRTVRVEDNHSYVSRLYGFPSEPHSREL---WVDVAENRQVKIHTILSNTHRQA--- 132
DB 2396 NFEVAFDEKKNVFEVYAPWCGCKGLAPWDKLGTYKEHQDI-VIAKNFEVAFDEN 2454
QY 133 SRVLSDFDFPYGHPRLQIATIGGFFMGDVIHRMLTATQYVAPLMANFPGYSNSTV 192
DB 2455 KNVFEVYAPWCGH-----CKQLAPAWDKLPGTYRDHENI 2489
QY 193 VYFONGTVFVYVQWHDVYVLOGWEDKGSFTFOALHHDGRIVFAFKEI-----PMSVP 243
DB 2490 VIAKN-----HDEIVNDPKDVLVLYYAPWCGCHKRLAPYQELADYANTSDVLIA 2542
QY 244 EISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEVH-----RI 283
DB 2543 KMDSTANEVAVKHSEFTLKF---FFPASADRTVIDYNGERTLDGFKFLESGMDSTAN 2599
QY 284 ELDSKVTSMASAVEFTPLPTCLQHRSCDACMSSDLT---FNCWCHVLCRCSSGFDYRQ 340
DB 2600 EYAVKHSEFTLKF---ASADRTVIDYNG-----ERTLDGFKFLE 2640
QY 341 EMDYGCQAQAEGRMCDFQDEHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKL 400
DB 2641 SGGMDSTANEVAVKHSEFTLKFPPASADRTVIDYNGERTLDGFKFLES-----2691
QY 401 NPYAGGDLQNNLS-----PKTKGTPVHLGTIVGLVAVLLVAAIILAGIYNGHPTS 453
DB 2692 ---GMDSTANEVAVKHSEFTLKFPPAGPGRTV-----IDYNGERTL 2732
QY 454 NAALFFIER-----RPHHPAMKFRSHPDHSTYAEVPSGHEK-EGF 494
DB 2733 DGFKKFLSGGMDSTANEVAVKHSEFTLKF---FPAGSRNVIDYNGERTLEGF 2785

RESULT 6
US-08-431-080-28
; Sequence 28, Application US/08431080
; Patent No. 5698686
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,080
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SN 08/326,781
; FILING DATE: October 20, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD:155/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1085 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-431-080-28

Query Match 3.5%; Score 93; DB 1; Length 1085;
Best Local Similarity 19.0%; Pred. No. 4.5;
Matches 88; Conservative 55; Mismatches 152; Indels 168; Gaps 24;

QY 56 SPDRTOISQDLGGGTFLAMDTLPDNRTRVVDNHSYVSRLYGFPSEPHSRELWVD--VAE 113
DB 333 NEDSGEIGTDEGE---DDLQ-----ILLEEQNIIVSEL-----QNDDELSDGSIHE 379
QY 114 ANRSQVK---IHTILSNTHRQAS-----RVVLSDFDFPYGHPRLQIATIGGFIFM 161
DB 380 EGSDPVEDAENKFLQNEYNQENGYDEEDEDEIMSDMPFEDP-----KFLNLYY 433
QY 162 GDVIRMLTATQYVAPLMAN-----FNPYSDNST 191
DB 434 GDSGPKLSLSL-PLMLNDEKLSKLKKAQKREQERKQRRKLYKKTKPSTRTTSN 492
QY 192 VYFONGTVFVYVQWHDVYVLOGWEDKGSFTFOALHHDGRIVFAFKEI-----EIPMSVPEISS 247
DB 493 V---DNDEYIF---NVFQSDDENSGHKKGRKSHIEHKNGKSNLKSNDLLEP 545
QY 248 SQHP---VKTGLSDAFMILNPSDPVPSRRRSIFEVHRIELDPKSVTSMASAVEFTPLPTCL 305
DB 546 STHSTVLNSGKYDS---SDD-----EYDNILLD-----VAHMP-----575
QY 306 QHRSCDACMSSDLTFCNSWCHVLCRCSSGFDYRQEMWMDYGCQAQAEGRMCDFQDEH 365
DB 576 ---SDDECESETSHTADTDEELRALDS-----DSLDTG-----ELDDYEDDDDD 619
QY 366 SA-----SPTSFSFYDGD---LTTTSSS-----LFDLSL 392
DB 620 SSVTVNVIDIDLDLDFDSFYHYDSDGSSSLSSNSDKNSGSKDKCKHDLLETVVYVDD 679
QY 393 TTEDDTKLPYAGGDLQNNLSPKTKG-----TPVHLGT 426
DB 680 STDEDDNLPP---PSSRSKNIGSKAKEIVSSNVVGLRPPKLG 719

RESULT 7
US-08-938-534-28
; Sequence 28, Application US/08938534
; Patent No. 5916752
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433

```


: CITY: Houston
: STATE: TEXAS
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/938,534
: FILING DATE: 26-SEP-1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/431,080
: FILING DATE:
: APPLICATION NUMBER: SN 08/326,781
: FILING DATE: October 20, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Parker, David L.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: ARCD:155/PAR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (713) 789-2679
: TELEX: 79-0924
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-938-534-28

Query Match 3.5%; Score 93; DB 2; Length 1085;

Best Local Similarity 19.0%; Pred. No. 4.5;
Matches 88; Conservative 55; Mismatches 152; Indels 168; Gaps 24;

QY 56 SEPDRQLSODLGGGTAMDTLPDNRTRVVDNHSYVSRLYGPPSEPHSRELWVD--VAE 113
DB 333 NEDSHGEIGTDLETGE---DDLPL-----ILEEEQNIVSEL-----QNDDELSDFGSIHE 379
QY 114 ANRSQVK--IHTILSNTHRQAS-----RVVLSDFPFYGHPLRQITATGGFIFM 161
DB 380 EGSDPVEDAENKFLQNEYNQENGDEDEDEIMSDMPFYEDP-----KEANLYYY 433
QY 162 GDVHRMLTATQYVAPLMA-----FNPQYSDNST 191
DB 434 GDGSEPKLSLSTSL-PLMLNDEKLSKLKKEAKKREQERKORRKLKTKQKSTRRTSN 492
QY 192 VVVFONGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYK-----EIPMSVPEISS 247
DB 493 V---DNDEYIF---NVFFQSDDENSGHKSCKGRHKSKEHIEHNKNSLIKSNDLLEP 545
QY 248 SQHP--VKTGLSDFMILNPSDPVPSRRRSIFEYHRIELDPKSVKTSMSAVEFTPLPTCL 305
DB 546 STHSTVLNSGKYDS-----SD-----EYDNLID-----VAHMP----- 575
QY 306 QHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDFODEDHD 365
DB 576 ---SDDECESESHDADTDEELRALDS-----DSLIDGT-----ELDDYEDDDDD 619
QY 366 SA-----SPDTSFSPYDGD---LTTSSS-----LFDLSL 392
DB 620 SSVTVFIDIDLDPSFYHSDSGSSLSISNSDKNSGSKCKKHDLLETVVVYVDE 679
QY 393 TTEDDTKLNPYAGGDLQNNLSFKTKG-----TPVHLGT 426
DB 680 STDEDDNLPP---PSSRSKNIGSKAKEIVSSNVVGLRPPKLT 719

RESULT 8

US-09-345-294-28

: Sequence 28, Application US/09345294
: Patent No. 6387619
: GENERAL INFORMATION:
: APPLICANT: Gottschling, Daniel E.
: Singer, Miriam S.
: TITLE OF INVENTION: Telomerase Compositions and Methods
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TEXAS
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/345,294
: FILING DATE: 30-Jun-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/431,080
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Parker, David L.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: ARCD:155/PAR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (713) 789-2679
: TELEX: 79-0924
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1085 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 28:
: US-09-345-294-28

Query Match 3.5%; Score 93; DB 4; Length 1085;
Best Local Similarity 19.0%; Pred. No. 4.5;
Matches 88; Conservative 55; Mismatches 152; Indels 168; Gaps 24;

QY 56 SEPDRQLSODLGGGTAMDTLPDNRTRVVDNHSYVSRLYGPPSEPHSRELWVD--VAE 113
DB 333 NEDSHGEIGTDLETGE---DDLPL-----ILEEEQNIVSEL-----QNDDELSDFGSIHE 379
QY 114 ANRSQVK--IHTILSNTHRQAS-----RVVLSDFPFYGHPLRQITATGGFIFM 161
DB 380 EGSDPVEDAENKFLQNEYNQENGDEDEDEIMSDMPFYEDP-----KEANLYYY 433
QY 162 GDVHRMLTATQYVAPLMA-----FNPQYSDNST 191
DB 434 GDGSEPKLSLSTSL-PLMLNDEKLSKLKKEAKKREQERKORRKLKTKQKSTRRTSN 492
QY 192 VVVFONGTVFVQWHDVYLGWEDKGSFTFQAALHHDGRIVFAYK-----EIPMSVPEISS 247
DB 493 V---DNDEYIF---NVFFQSDDENSGHKSCKGRHKSKEHIEHNKNSLIKSNDLLEP 545
QY 248 SQHP--VKTGLSDFMILNPSDPVPSRRRSIFEYHRIELDPKSVKTSMSAVEFTPLPTCL 305
DB 546 STHSTVLNSGKYDS-----SD-----EYDNLID-----VAHMP----- 575
QY 306 QHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDYRQEMDYGCAQAEGRMCEDFODEDHD 365
DB 576 ---SDDECESESHDADTDEELRALDS-----DSLIDGT-----ELDDYEDDDDD 619
QY 366 SA-----SPDTSFSPYDGD---LTTSSS-----LFDLSL 392

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELEPHONE: 904-375-8100
TELEFAX: 904-375-5800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1220 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
INDIVIDUAL ISOLATE: 86Q3
IMMEDIATE SOURCE:
LIBRARY: Lambdagem (TM) - 11 library of Luis
LIBRARY: Foncerrada
CLONE: 86Q3c
US-08-611-928-43

Query Match 3.4%; Score 92.5; DB 2; Length 1220;
Best Local Similarity 20.7%; Pred. No. 6.1;
Matches 74; Conservative 37; Mismatches 108; Indels 139; Gaps 18;

QY 20 SPQAGHDEGPGSGW---AAKGTGVRGNRRRARESPGHVSEPDRTQISDQLGGGTL-AMD 75
DB 442 TPQGA-----SGWNTNLMRGVSGLSFLQR-----DGTSLSAGMGGGFADTIY 485
QY 76 TLPDNRTRVVEDNHSYVSRLYG---PSEPHSRELWVDVAEANKRSQVKIHTILSNTHRQ 131
DB 486 SLP-----ATHYLSYLYGTPYQTSNYSYGHVGVSTPQEAATLPNII-----529
QY 132 ASRVVLSDFPFYGHPLRQITATGGIFM-----GDVIHRLMTATQYVAPLMANFNG- 185
DB 530 -----GQDEQGNVSTMGFFPEKASYGTVVKEWLNANAM-----KLSPGQ 571
QY 186 -----YSDNSTVYVFDNGTVFVQWMDHVYLOGWEDKG-----SF 219
DB 664 -----DRIEFVPK-----IQFQCDNNLHCDGNPVDCTCF-CCVCTSLTDC 706

RESULT 11
US-09-173-891-43
Sequence 43, Application US/09173891
Patent No. 6077937
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Kennedy, M. Keith
APPLICANT: Randall, John Brooks
APPLICANT: Meier, Henry
APPLICANT: Uick, Heidi Jane
APPLICANT: Foncerrada, Luis
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schwab, George E.
APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 6077937el Bacillus thuringiensis Toxins Active

TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/158,232
FILING DATE:
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1220 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
INDIVIDUAL ISOLATE: 86Q3
IMMEDIATE SOURCE:
LIBRARY: Lambdagem (TM) - 11 library of Luis
LIBRARY: Foncerrada
CLONE: 86Q3c
US-09-173-891-43

Query Match 3.4%; Score 92.5; DB 3; Length 1220;
Best Local Similarity 20.7%; Pred. No. 6.1;
Matches 74; Conservative 37; Mismatches 108; Indels 139; Gaps 18;

QY 20 SPQAGHDEGPGSGW---AAKGTGVRGNRRRARESPGHVSEPDRTQISDQLGGGTL-AMD 75
DB 442 TPQGA-----SGWNTNLMRGVSGLSFLQR-----DGTSLSAGMGGGFADTIY 485
QY 76 TLPDNRTRVVEDNHSYVSRLYG---PSEPHSRELWVDVAEANKRSQVKIHTILSNTHRQ 131
DB 486 SLP-----ATHYLSYLYGTPYQTSNYSYGHVGVSTPQEAATLPNII-----529
QY 132 ASRVVLSDFPFYGHPLRQITATGGIFM-----GDVIHRLMTATQYVAPLMANFNG- 185
DB 530 -----GQDEQGNVSTMGFFPEKASYGTVVKEWLNANAM-----KLSPGQ 571
QY 186 -----YSDNSTVYVFDNGTVFVQWMDHVYLOGWEDKG-----SF 219
DB 572 SIGIPITNVTKHNYQVRCRYASNS-----DNPVFNV-----DTGGANPIFQOI 615

QY 220 TFOAALHDGRI-----VFAYKEI-PMSVPEISSQHPVKTKGLSDAFMILNPSDPVPSR 273
 Db 616 NFASTVDSNMGVRENGYVYVVKSLKTEIAGSFYVHTNQGSSDLFL-----663
 QY 274 RRSIFEYHRIELDSPKVTSMASAVEFTPLPTCLOHRSODACMSDDLTFNCSWCHVLQRC 331
 Db 664 -----DRIEFVFK-----IQQPCDNNLHCDNPNVDTCDF-CCVCTSLTDC 706

RESULT 12
 US-08-484-993B-18
 ; Sequence 18, Application US/08484993B
 ; Patent No. 5837497
 ; GENERAL INFORMATION:
 ; APPLICANT: Harris Ph.D., Jeffrey D.
 ; APPLICANT: Hsu, Kuang T.
 ; APPLICANT: Podolski, Joseph S.
 ; TITLE OF INVENTION: Materials and Methods for Immunocontraception
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,993B
 ; FILING DATE: 09-NOV-1993
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/012,990
 ; FILING DATE: 29-JAN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/973,341
 ; FILING DATE: 09-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; REFERENCE/DOCKET NUMBER: 31745
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6653
 ; TELEFAX: 312/474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 424 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-484-993B-18

Query Match 3.4%; Score 90.5; DB 2; Length 424;
 Best Local Similarity 19.5%; Pred. No. 1.8;
 Matches 86; Conservative 67; Mismatches 165; Indels 123; Gaps 22;

QY 76 TLPDNRTRVDNHSYV-----SRLYGPSE-----PHSRELWV--DVAEANSQV 119
 Db 33 SLPSPSVVVECRHAWLVVNVSKNLFGRVLRPADLTLPENCEPLISGSDSDTVRFEV 92
 QY 120 KHTLTLSNTHROASRVVLSFDPFVGHPLROITATGTFIFMGDVIHRLMTATQYVAPLM 179
 Db 93 ELHKCGNSQVVEDALVYSTLLNPRMGNLSI-----LRTNRAEVPDIE 137
 QY 180 ANFNPCYSDNS-----TVVYFDNGTVFVQMDHVVYLCQW-EDKGSFTFOAA-L 225
 Db 138 CRY-PHNSVNSEALPTWVFPRTMTLSEKLAFLSLR---LMEEDWGSEKQSPTEQLGDL 193

QY 226 HHGDRIVFAYKEIPMSV-----PEISSQHP-----VKTGLSDAFMILNPS 267
 Db 194 AHLQAEVHTGRHIPURLEFVDYCVATLTDPQNASPHHTIVDFHGLVDGLSDASSAFKAPR 253
 QY 268 DVPESRRRSIFEYHRIELDSPKVTSMASAVEFTPLPTCLOHRSODACMSDDLTF--- 320
 Db 254 PRPETLQFTVDTFH-FANDPRNMIYITCLHKVTPASRVPDQL-NKACSFIKSSNRWFPE 311
 QY 321 -----NCSWCHVLQRCSSGDEDRYQENMDYGCQAEAGRMCEDFQDEHDSASPDTSFS 374
 Db 312 GPADICNC-----CNKG-----SCGLQGRSWRLSHLDRPHWKASNRHRV 352
 QY 375 PYDGDLTITSSSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTIVGIVLAV 434
 Db 353 TEEADI-TVGPLIFLKG-----AADRGVEGTSP-----HTSVMVVGIGLAT 392

QY 435 L-LVAAIILAGIYINGHPTS 453
 Db 393 VLSLTATIVGLARRHHTAS 413

RESULT 13
 US-08-484-158B-18
 ; Sequence 18, Application US/08484158B
 ; Patent No. 5976545
 ; GENERAL INFORMATION:
 ; APPLICANT: Harris Ph.D., Jeffrey D.
 ; APPLICANT: Hsu, Kuang T.
 ; APPLICANT: Podolski, Joseph S.
 ; TITLE OF INVENTION: Pharmaceutical Compositions for
 ; IMMUNOCONTRACEPTION
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,158B
 ; FILING DATE: 07-JUNE-95
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/149,223
 ; FILING DATE: 09-NOV-93
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/012,990
 ; FILING DATE: 29-JAN-93
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/973,341
 ; FILING DATE: 09-NOV-92
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.
 ; REGISTRATION NUMBER: 36,107
 ; REFERENCE/DOCKET NUMBER: 32794
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6653
 ; TELEFAX: 312/474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 424 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-484-158B-18

Query Match 3.4%; Score 90.5; DB 2; Length 424;
Best Local Similarity 19.5%; Pred. No. 1.8;
Matches 86; Conservative 67; Mismatches 165; Indels 12

QY	76	TLPDNRTVRVEDNHYSYV-----SRLYGPSE----
Db	33	SLPSPSVYVECRHAWLVNVSKNLFGTGRVLRPADLTGPEENCEPLTSGSDSDTVREVF 92
QY	120	KIHITLSNTURQASRVVSLDPFPYGHPLRQIATIATGTFIFMGDVIHRMLTAIQYVAPLM 179
Db	93	ELHKCGNSVQVTEDALVYSTFLLNPRPMGNLST-----LRTNRAEVPTE 137
QY	180	ANFNPGYSDNS-----TVYFDNGTFFVVOVDHYVLQGW-EDKGSFTTFOAA-L 225
Db	138	CRY-PRHSNVSSAEALLPTWPFFTMLSEEKLAFSLR--LMBEDWGSEKQSFTFOLGDL 193
QY	226	HHDGRIVFAKEIPMSV-----PEISSQH-----VKTGLSDAEMIINPSP 267
Db	194	AHLQAEVHTGRHPIRLRFVDYCVATLTPDONASPHHTIVDFHGCLVDGLDSASSAFKAPR 253
QY	268	DVPSRRRSIFEYHRIELOPSKVTSMSA-VETFP--LptCLOHRSCDACWSSDLTF--- 320
Db	254	PRPETLQFTVDTEH-FANDERNWIYTCHLKVTASRPVOL-NKACSFIKSNRRPFVPE 311
QY	321	-----NCSWCHVLQRCSGFDRYQEWMDCGAQEAEGRMCEDFODEDHDSASPDTSES 374
Db	312	GPAIDCM-----CNKG-----SCGLQRSWRLSHLDRPWHKMASRRNRVV 352
QY	375	PYDGDLATTSSSLFDISLTTEDDTKLNPYAGDDGLONNLSPKTKTGVHLGTLVGIVLAV 434
Db	353	TEADII-TVGPLFILOK-----AADRGVESTSP-----HTSVNMVGI GLAT 392
QY	435	L--LVAAILIAGIYINGHPTS 453
Db	393	VLSUTLATIIVGLARRRHHTAS 413

RESULT 14
 US-08-484-596A-18
 ; Sequence 18, Application US/08484596A
 ; Patent No. 5981228
 ; GENERAL INFORMATION:
 ; APPLICANT: Harris Ph.D., Jeffrey D.
 ; APPLICANT: Hsu, Kuang T.
 ; APPLICANT: Podolski, Joseph S.
 ; TITLE OF INVENTION: Materials and Methods for Immunocontraception
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,596A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/149,223
 ; FILING DATE: 11-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/973,341
 ; FILING DATE: 09-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clough, David W.

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; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-596A-18

Query Match 3.4%; Score 90.5; DB 2; Length 424;
Best Local Similarity 19.5%; Pred. No. 1.8;
Matches 86; Conservative 67; Mismatches 165; Indels 123; Gaps 22;

QY 76 TLPDNRTRVVDNHSYV-----SRLYGPE-----PHSRELAV--DVAEANRSQV 119
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 33 SLSPSPVVVECHRWLVVNVKNLFTGLRLVRPADLTLPENCEPLISGSDSDTTRFEV 92
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 120 KIHTILSNTHROASRVVLSDFDPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLM 179
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 93 ELHKCGNSQVQTDALVYSTFLHLNPRPMGNLSI-----LRTNRAEVPPIE 137
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 180 ANENPGVSDNS-----TVVYFDNGTVFVQWDHVYLOGW--EDKGSFTFOAA--L 225
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 138 CRY-PRISNVSSRAILPTVPFRITMLSEKLAFLSLR---LMEEDWGSEKQSPFTQLGDL 193
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 226 HHQGRIVFAYKEIPMSV-----PEISSQHP-----VKTGLSDAFMILNPSP 267
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 194 AHLQAEVHTGRHPLRLFDVYCVATLTPDQNASPHHTIVDFHGLCLVDGLSDASSAFKAPR 253
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 268 DVPESRRSITFEYHRIELDSPKVTMSA-VEFTP---LPTCLOHRSCDCACMSSDLTF--- 320
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 254 PRPTIQTVDTHF--FANDPRNNIYITICHUKVTPASRVPDQL--NKACSFIKSSNRWFPVE 311
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 321 -----NCSMCHVLQRCSSGFDRYQROEMDYGCAQAEGRMCEDFQDEHDSDASPTDTSFS 374
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 312 GPADICNC-----CNKG-----SCLOGRSWRLSHLDPRPHKMASRNRHV 352
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 375 PYDGLTITSSSIFDSLTTEDTKLNPYAGGGLQNNLSPKTKGTPVHLGTIVGIVLAV 434
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 353 TEEADI--TVGLPIFLGK-----AADRGVEGSTSP-----HTSVWVGIGLAT 392
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

QY 435 L--LVAAILAGIYINGHPTS 453
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 393 VLSLTATIVLGLARRHHTAS 413
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

RESULT 15
US-08-480-150A-18
; Sequence 18, Application US/08480150A
; Patent No. 5989550
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immunocontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,150A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,223
; FILING DATE: 09-NOV-1993
; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-480-150A-18

Query Match      3.4%; Score 90.5; DB 2; Length 424;
Best Local Similarity 19.5%; Pred. No. 1.8;
Matches 86; Conservative 67; Mismatches 165; Indels 123; Gaps 22;

QY 76 TLPNRTRVEDNHSYYV-----SRLYGPSE-----PHSRELWV--DVAEANKRSQV 119
DB 33 SLSPSSPVVVECRHAWLVNVVSKNLFGTGLVRPADLTGLPENCEPLISGSDSDTVERFEV 92
QY 120 KHTILSNTHRQASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLM 179
DB 93 ELHKGNSVQVTEALVYSTFLLNPRPMGNLSI-----LRTNRAEVP 137
QY 180 ANFNPGYSDNS-----TVYFDNGTVEVQWMDHYVLOGW-EDKGSFTFOAA-L 225
DB 138 CRY-PRHSNVSSAAILPTWPFRTTLMSEKLAFLSLR---LMEEDWGSEKQSPTFQLGDL 193
QY 226 HDGRIVFAYKEIPMSV-----PEISSQHP-----VKTGLSDAFMLNPSP 267
DB 194 AHLQAEVHTGRHILRLRFVYCVATLTPDQNASPHHTIVDFHGCCLVDGLSDASSAFKAPR 253
QY 268 DVPESRRRSIFEYHRIELDPKSVTSMAS-VFETP---LPTCLOHRSCDACMSSDLTF--- 320
DB 254 PRPETLQFTVDTFH-FANDPRNMIYITCHLKVTPASRPDOL-NKACSFIKSSNRWFPVE 311
QY 321 -----NCSWCHVLQRCSSGFDRYQEWMDYGCQAQEAEGRMCEDFQDEHDHDSASPTSF 374
DB 312 GPADICNC-----CNKG-----SCGLQGRSWRLSHLDRPWHKMASRRRHV 352
QY 375 PYDGLTITSSSLFDLTEDDKLNYPAGDGLONNLSPKTKGTPVHLGTIVGIVLAV 434
DB 353 TEEADI-TVGPLIFLGK-----AADRGVEGSTSP-----HTSVMVVIGLAT 392
QY 435 L--LVAAILAGIYINGHPTS 453
DB 393 VLSLTLATIVLGLARRHTAS 413
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Job time : 26 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using 'sw model

Run on: April 22, 2003, 16:15:46 ; Search time 31 Seconds
(without alignments)
474.563 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 500

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents_AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	7	1.4	193	2	US-08-564-972-8
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6	7	1.4	194	1	US-08-148-058A-29
7	7	1.4	194	1	US-08-478-042-27
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9	7	1.4	194	2	US-08-645-215-27
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14	7	1.4	432	4	US-09-306-595C-8
15	7	1.4	471	1	US-08-203-905B-2
16	7	1.4	472	1	US-08-203-905B-14
17	7	1.4	498	4	US-09-172-952-26
18	7	1.4	520	4	US-09-326-203A-2
19	7	1.4	535	2	US-08-564-972-1
20	7	1.4	535	4	US-09-171-969-9
21	7	1.4	535	4	US-09-250-131-2
22	7	1.4	599	2	US-08-954-333-7
23	7	1.4	693	1	US-08-553-279-2
24	7	1.4	794	1	US-08-188-228-60
25	7	1.4	794	1	US-08-332-643-54
26	7	1.4	794	1	US-08-332-638-60
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40	6	1.2	9	2	US-08-340-283-28	Sequence 28, Appl
41	6	1.2	9	2	US-08-340-283-31	Sequence 31, Appl
42	6	1.2	9	2	US-08-340-283-62	Sequence 62, Appl
43	6	1.2	10	6	5196523-16	Patent No. 5196523
44	6	1.2	11	5	PCT-US92-01433A-6	Sequence 6, Appli
45	6	1.2	15	1	US-07-859-291C-37	Sequence 37, Appl
46	6	1.2	15	1	US-08-343-606-1	Sequence 1, Appli
47	6	1.2	15	2	US-08-888-497-1	Sequence 1, Appli
48	6	1.2	15	4	US-09-362-230-1	Sequence 1, Appli
49	6	1.2	15	5	PCT-US93-06751-57	Sequence 57, Appl
50	6	1.2	15	5	PCT-US94-07926-1	Sequence 1, Appli
51	6	1.2	24	4	US-08-905-223-498	Sequence 498, App
52	6	1.2	27	1	US-07-668-648-12	Sequence 12, Appl
53	6	1.2	27	2	US-08-429-998-12	Sequence 12, Appl
54	6	1.2	27	2	US-08-751-305-25	Sequence 25, Appl
55	6	1.2	27	2	US-08-431-333-12	Sequence 12, Appl
56	6	1.2	27	5	PCT-US91-02321-12	Sequence 12, Appl
57	6	1.2	30	3	US-08-809-397-18	Sequence 18, Appl
58	6	1.2	30	4	US-09-425-597-18	Sequence 18, Appl
59	6	1.2	30	5	PCT-US95-12502-18	Sequence 18, Appl
60	6	1.2	34	2	US-08-751-305-6	Sequence 6, Appli
61	6	1.2	40	3	US-08-926-842B-52	Sequence 52, Appl
62	6	1.2	58	4	US-09-271-438A-15	Sequence 15, Appl
63	6	1.2	61	2	US-08-359-222-2	Sequence 2, Appli
64	6	1.2	61	3	US-09-094-563-2	Sequence 2, Appli
65	6	1.2	68	4	US-08-905-223-369	Sequence 369, App
66	6	1.2	80	1	US-08-464-164-4	Sequence 4, Appli
67	6	1.2	80	1	US-08-338-057-4	Sequence 4, Appli
68	6	1.2	80	2	US-08-668-416-4	Sequence 4, Appli
69	6	1.2	82	4	US-08-905-223-449	Sequence 449, App
70	6	1.2	84	4	US-08-905-223-404	Sequence 404, App
71	6	1.2	93	4	US-08-936-165A-340	Sequence 340, App
72	6	1.2	100	1	US-08-158-189-7	Sequence 7, Appli
73	6	1.2	123	2	US-08-626-685A-10	Sequence 10, Appl
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75	6	1.2	125	3	US-08-513-974B-346	Sequence 346, App
76	6	1.2	125	3	US-08-513-974B-347	Sequence 347, App
77	6	1.2	129	6	5196523-10	Patent No. 5196523
78	6	1.2	139	4	US-08-444-818-174	Sequence 174, App
79	6	1.2	148	2	US-08-888-497-36	Sequence 36, Appl
80	6	1.2	148	5	PCT-US94-07926-36	Sequence 36, Appl
81	6	1.2	148	5	US-09-615-192A-279	Sequence 279, App
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83	6	1.2	161	1	US-08-451-747-13	Sequence 13, Appl
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95	6	1.2	199	4	US-09-134-001C-3833	Sequence 3833, Ap
96	6	1.2	204	4	US-09-029-603-3	Sequence 3, Appli
97	6	1.2	206	4	US-09-134-001C-3929	Sequence 3929, Ap
98	6	1.2	218	4	US-09-651-656-105	Sequence 105, App
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100	6	1.2	218	4	US-09-651-656-105	Sequence 105, App

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104	1.2	223	3	US-08-820-970-2	Sequence 2, Appli	177	6	1.2	394	5	PCT-US94-03705-5	Sequence 5, Appli
105	1.2	223	4	US-09-724-864-46	Sequence 46, Appli	178	6	1.2	399	1	US-08-414-926A-5	Sequence 5, Appli
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112	1.2	272	3	US-08-908-332-8	Sequence 8, Appli	185	6	1.2	407	4	US-08-861-774E-28	Sequence 28, Appli
113	1.2	274	4	US-09-149-476-358	Sequence 358, App	186	6	1.2	410	4	US-09-258-754-450	Sequence 450, App
114	1.2	276	4	US-09-485-549-2	Sequence 2, Appli	187	6	1.2	410	4	US-09-258-754-451	Sequence 451, App
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136	1.2	350	4	US-09-576-160B-5	Sequence 5, Appli	209	6	1.2	451	4	US-09-215-649A-4	Sequence 4, Appli
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153	1.2	372	4	US-08-665-034A-2	Sequence 2, Appli	226	6	1.2	489	1	US-08-801-718-5	Sequence 5, Appli
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156	1.2	375	2	US-08-102-385G-10	Sequence 10, Appli	229	6	1.2	489	4	US-09-480-718-46	Sequence 46, Appli
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160	1.2	379	4	US-09-817-856-15	Sequence 15, Appli	233	6	1.2	499	4	US-09-239-662-4	Sequence 4, Appli
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162	1.2	383	1	US-08-457-135-2	Sequence 2, Appli	235	6	1.2	509	2	US-08-559-505-4	Sequence 4, Appli
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164	1.2	386	1	US-08-520-519-3	Sequence 3, Appli	237	6	1.2	509	2	US-08-890-980-4	Sequence 4, Appli
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170	1.2	388	4	US-09-363-745-7	Sequence 7, Appli	243	6	1.2	509	4	US-09-241-581B-8	Sequence 8, Appli
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173	1.2	390	1	US-08-395-939A-1	Sequence 1, Appli	246	6	1.2	509	5		

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250	6	1.2	524	4	US-09-299-662-1	Sequence 1, Appli	323	6	1.2	4	US-09-232-191-29	Sequence 29, Appl
251	6	1.2	527	4	US-09-134-001C-3358	Sequence 3358, Ap	324	6	1.2	4	US-09-232-200-79	Sequence 79, Appl
252	6	1.2	529	3	US-08-821-984-6	Sequence 6, Appli	325	6	1.2	4	US-09-232-200-97	Sequence 97, Appl
253	6	1.2	529	3	US-08-821-984-8	Sequence 8, Appli	326	6	1.2	4	US-09-232-197-79	Sequence 97, Appl
254	6	1.2	529	4	US-09-329-749-6	Sequence 6, Appli	327	6	1.2	4	US-09-232-197-97	Sequence 97, Appl
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258	6	1.2	546	1	US-08-487-990A-99	Sequence 99, Appl	331	6	1.2	1	US-08-441-139-11	Sequence 11, Appl
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261	6	1.2	546	2	US-08-478-373-99	Sequence 99, Appl	334	6	1.2	663	US-08-441-139-7	Sequence 7, Appli
262	6	1.2	546	3	US-08-474-671-99	Sequence 99, Appl	335	6	1.2	666	US-08-441-139-16	Sequence 16, Appl
263	6	1.2	546	3	US-08-483-577A-99	Sequence 99, Appl	336	6	1.2	668	US-09-930-181-2	Sequence 2, Appli
264	6	1.2	546	4	US-08-897-438-99	Sequence 99, Appl	337	6	1.2	670	US-08-363-208-2	Sequence 2, Appli
265	6	1.2	546	4	US-08-637-654-99	Sequence 99, Appl	338	6	1.2	670	US-09-137-478-2	Sequence 2, Appli
266	6	1.2	546	4	US-08-649-518-99	Sequence 99, Appl	339	6	1.2	671	US-08-426-125-8	Sequence 8, Appli
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269	6	1.2	547	1	US-08-217-438-2	Sequence 2, Appli	342	6	1.2	682	US-08-441-139-5	Sequence 5, Appli
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273	6	1.2	547	2	US-08-710-584-2	Sequence 2, Appli	346	6	1.2	704	US-09-370-838-191	Sequence 191, App
274	6	1.2	547	2	US-08-710-584-5	Sequence 5, Appli	347	6	1.2	726	US-09-502-812-10	Sequence 10, Appl
275	6	1.2	549	4	US-09-134-001C-2973	Sequence 2973, Ap	348	6	1.2	726	US-09-511-507-10	Sequence 10, Appl
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277	6	1.2	550	2	US-08-795-303-4	Sequence 4, Appli	350	6	1.2	731	US-09-185-160-11	Sequence 11, Appl
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279	6	1.2	551	6	5198359-2	Patent No. 5198359	352	6	1.2	734	US-09-185-160-13	Sequence 13, Appl
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281	6	1.2	563	4	US-09-422-936-79	Sequence 79, Appl	354	6	1.2	790	US-08-537-361E-8	Sequence 8, Appli
282	6	1.2	573	4	US-09-042-785A-2	Sequence 2, Appli	355	6	1.2	790	US-08-817-707-6	Sequence 6, Appli
283	6	1.2	582	2	US-08-403-852D-20	Sequence 20, Appl	356	6	1.2	791	US-08-537-361E-4	Sequence 4, Appli
284	6	1.2	582	3	US-08-510-646B-21	Sequence 21, Appl	357	6	1.2	792	US-08-326-670A-2	Sequence 2, Appli
285	6	1.2	582	4	US-09-231-818-20	Sequence 20, Appl	358	6	1.2	792	US-08-678-039A-40	Sequence 40, Appl
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287	6	1.2	591	3	US-08-996-139-2	Sequence 2, Appli	360	6	1.2	792	US-08-990-470A-2	Sequence 2, Appli
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292	6	1.2	593	1	US-07-961-522-4	Sequence 4, Appli	365	6	1.2	796	US-09-757-014-2	Sequence 2, Appli
293	6	1.2	593	1	US-08-217-438-4	Sequence 4, Appli	366	6	1.2	801	US-09-104-070-2	Sequence 2, Appli
294	6	1.2	593	1	US-08-217-438-5	Sequence 5, Appli	367	6	1.2	811	US-09-199-637A-93	Sequence 93, Appl
295	6	1.2	593	1	US-08-487-890A-100	Sequence 100, App	368	6	1.2	819	US-09-651-656-15	Sequence 15, Appl
296	6	1.2	593	1	US-08-321-978-4	Sequence 4, Appli	369	6	1.2	819	US-09-650-855-15	Sequence 15, Appl
297	6	1.2	593	2	US-08-710-584-4	Sequence 4, Appli	370	6	1.2	839	US-09-197-636-2	Sequence 2, Appli
298	6	1.2	593	2	US-08-478-435-100	Sequence 100, App	371	6	1.2	839	US-09-197-636-4	Sequence 4, Appli
299	6	1.2	593	2	US-08-337-483-100	Sequence 100, App	372	6	1.2	839	US-09-197-636-8	Sequence 8, Appli
300	6	1.2	593	3	US-08-478-373-100	Sequence 100, App	373	6	1.2	839	US-09-235-451-34	Sequence 34, Appl
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302	6	1.2	593	3	US-08-483-577A-100	Sequence 100, App	375	6	1.2	844	US-09-422-936-51	Sequence 51, Appl
303	6	1.2	593	4	US-08-897-438-100	Sequence 100, App	376	6	1.2	848	US-08-976-255-10	Sequence 10, Appl
304	6	1.2	593	4	US-08-637-654-100	Sequence 100, App	377	6	1.2	864	US-09-604-978-11	Sequence 11, Appl
305	6	1.2	593	4	US-08-649-518-100	Sequence 100, App	378	6	1.2	877	US-08-072-574-12	Sequence 12, Appl
306	6	1.2	600	6	US-08-836-620A-16	Sequence 16, Appl	379	6	1.2	877	US-08-367-264-12	Sequence 12, Appl
307	6	1.2	603	4	US-09-330-181-17	Sequence 17, Appl	380	6	1.2	877	US-09-153-757-12	Sequence 12, Appl
308	6	1.2	607	2	US-08-472-534-5	Sequence 5, Appli	381	6	1.2	886	US-09-422-936-77	Sequence 77, Appl
309	6	1.2	608	4	US-09-130-491-13	Sequence 13, Appl	382	6	1.2	890	US-09-513-783A-174	Sequence 174, App
310	6	1.2	612	3	US-09-295-186-16	Sequence 16, Appl	383	6	1.2	892	US-09-422-936-75	Sequence 75, Appl
311	6	1.2	616	3	US-08-996-139-6	Sequence 6, Appli	384	6	1.2	899	US-09-422-936-71	Sequence 71, Appl
312	6	1.2	616	4	US-08-995-659-6	Sequence 6, Appli	385	6	1.2			
313	6	1.2	616	4	US-09-215-649A-6	Sequence 6, Appli	386	6	1.2			
314	6	1.2	616	4	US-09-134-001C-3646	Sequence 3646, Ap	387	6	1.2			
315	6	1.2	616	4	US-09-577-780-6	Sequence 6, Appli	388	6	1.2			
316	6	1.2	641	1	US-08-441-139-4	Sequence 4, Appli	389	6	1.2			
317	6	1.2	641	2	US-08-873-479-42	Sequence 42, Appl	390	6	1.2			
318	6	1.2	644	4	US-08-797-358B-3	Sequence 3, Appli	391	6	1.2			
319	6	1.2	644	4	US-09-300-909-18	Sequence 18, Appl	392	6	1.2			

393	6	1.2	905	1	US-08-072-574-2	Sequence 2, Appli	466	6	1.2	1581	4	US-09-208-716-4	Sequence 4, Appli
394	6	1.2	906	1	US-08-486-270-2	Sequence 2, Appli	467	6	1.2	1582	2	US-08-404-531B-9	Sequence 9, Appli
395	6	1.2	906	3	US-08-367-264-2	Sequence 2, Appli	468	6	1.2	1582	3	US-08-476-900A-9	Sequence 9, Appli
396	6	1.2	906	4	US-09-153-757-2	Sequence 2, Appli	469	6	1.2	1582	3	US-08-488-546A-9	Sequence 9, Appli
397	6	1.2	906	5	PCT-US91-09422-17	Sequence 17, Appl	470	6	1.2	1582	4	US-08-726-320-5	Sequence 5, Appli
398	6	1.2	914	4	US-09-134-001C-5208	Sequence 5208, Ap	471	6	1.2	1582	4	US-09-208-716-5	Sequence 5, Appli
399	6	1.2	935	1	US-08-006-676B-1	Sequence 1, Appli	472	6	1.2	1651	1	US-08-447-411-2	Sequence 2, Appli
400	6	1.2	935	1	US-08-282-845-2	Sequence 2, Appli	473	6	1.2	1745	2	US-09-031-485-33	Sequence 33, Appl
401	6	1.2	935	2	US-08-428-414A-3	Sequence 3, Appli	474	6	1.2	1745	2	US-08-847-429A-33	Sequence 33, Appl
402	6	1.2	935	5	PCT-US94-00324-1	Sequence 1, Appli	475	6	1.2	1745	3	US-09-065-474-33	Sequence 33, Appl
403	6	1.2	960	4	US-09-422-936-45	Sequence 45, Appl	476	6	1.2	1745	4	US-09-557-034-33	Sequence 33, Appl
404	6	1.2	961	4	US-09-422-936-49	Sequence 49, Appl	477	6	1.2	2343	4	US-09-324-867-2	Sequence 2, Appli
405	6	1.2	964	4	US-09-422-936-53	Sequence 53, Appl	478	6	1.2	2532	4	US-09-215-694-10	Sequence 10, Appl
406	6	1.2	967	4	US-09-130-491-2	Sequence 2, Appli	479	6	1.2	2549	4	US-08-471-112A-3	Sequence 3, Appli
407	6	1.2	984	4	US-09-287-354-2	Sequence 2, Appli	480	6	1.2	2549	5	PCT-US95-06722-12	Sequence 12, Appli
408	6	1.2	1005	4	US-09-770-170-4	Sequence 4, Appli	481	6	1.2	2616	6	5206163-3	Patent No. 5206163
409	6	1.2	1038	4	US-08-334-179A-2	Sequence 2, Appli	482	6	1.2	2890	6	US-09-413-814-67	Sequence 67, Appl
410	6	1.2	1038	4	US-08-334-179A-8	Sequence 8, Appli	483	6	1.2	3025	6	5223423-3	Patent No. 5223423
411	6	1.2	1056	2	US-08-687-289A-7	Sequence 7, Appli	484	6	1.2	3031	1	US-07-689-008-2	Sequence 2, Appli
412	6	1.2	1056	2	US-08-687-289A-8	Sequence 8, Appli	485	6	1.2	3461	4	US-09-334-220-2	Sequence 2, Appli
413	6	1.2	1075	2	US-08-993-228-19	Sequence 19, Appl	486	6	1.2	3798	3	US-09-335-409-6	Sequence 6, Appli
414	6	1.2	1093	3	US-08-545-860D-55	Sequence 55, Appl	487	6	1.2	3798	4	US-09-568-102-6	Sequence 6, Appli
415	6	1.2	1093	5	PCT-US94-04496-55	Sequence 55, Appl	488	6	1.2	3798	4	US-09-567-969-6	Sequence 6, Appli
416	6	1.2	1142	4	US-09-106-075A-89	Sequence 89, Appl	489	6	1.2	3798	4	US-09-568-480-6	Sequence 6, Appli
417	6	1.2	1147	1	US-08-131-365B-38	Sequence 38, Appl	490	6	1.2	3798	4	US-09-568-486-6	Sequence 6, Appli
418	6	1.2	1147	2	US-08-668-123-38	Sequence 38, Appl	491	6	1.2	3798	4	US-09-568-472-6	Sequence 6, Appli
419	6	1.2	1180	1	US-08-072-574-8	Sequence 8, Appli	492	6	1.2	3798	4	US-09-567-899-6	Sequence 6, Appli
420	6	1.2	1180	3	US-08-367-264-8	Sequence 8, Appli	493	6	1.2	4551	3	US-09-320-878-1	Sequence 1, Appli
421	6	1.2	1180	3	US-08-367-264-8	Sequence 8, Appli	494	6	1.2	4613	4	US-09-105-537-31	Sequence 31, Appl
422	6	1.2	1180	4	US-08-660-148-2	Sequence 2, Appli	495	6	1.2	7257	3	US-09-335-409-5	Sequence 5, Appli
423	6	1.2	1180	4	US-09-153-757-8	Sequence 8, Appli	496	6	1.2	7257	4	US-09-568-102-5	Sequence 5, Appli
424	6	1.2	1186	1	US-08-485-568A-4	Sequence 4, Appli	497	6	1.2	7257	4	US-09-567-969-5	Sequence 5, Appli
425	6	1.2	1186	1	US-08-357-698-6	Sequence 6, Appli	498	6	1.2	7257	4	US-09-568-480-5	Sequence 5, Appli
426	6	1.2	1186	2	US-08-590-554A-4	Sequence 4, Appli	499	6	1.2	7257	4	US-09-568-486-5	Sequence 5, Appli
427	6	1.2	1186	2	US-09-184-223-4	Sequence 4, Appli	500	6	1.2	7257	4	US-09-568-472-5	Sequence 5, Appli
428	6	1.2	1186	5	PCT-US93-12682-6	Sequence 6, Appli	501	6	1.2	7257	4	US-09-567-899-5	Sequence 5, Appli
429	6	1.2	1189	4	US-09-287-354-3	Sequence 3, Appli	502	6	1.2	11877	4	US-09-105-537-6	Sequence 6, Appli
430	6	1.2	1189	4	US-09-287-354-4	Sequence 4, Appli	503	5	1.0	5	2	US-08-679-865-21	Sequence 21, Appl
431	6	1.2	1194	4	US-08-538-526-1	Sequence 1, Appli	504	5	1.0	5	2	US-08-680-876-21	Sequence 21, Appl
432	6	1.2	1199	1	US-08-041-538-2	Sequence 2, Appli	505	5	1.0	5	4	US-08-974-549A-173	Sequence 173, App
433	6	1.2	1199	1	US-08-463-642-2	Sequence 2, Appli	506	5	1.0	5	4	US-09-263-975-21	Sequence 21, Appl
434	6	1.2	1199	1	US-08-455-602-2	Sequence 2, Appli	507	5	1.0	5	4	US-08-665-643A-48	Sequence 48, Appl
435	6	1.2	1199	2	US-08-465-157-2	Sequence 2, Appli	508	5	1.0	5	4	US-08-665-643A-49	Sequence 49, Appl
436	6	1.2	1199	5	PCT-US91-09422-2	Sequence 2, Appli	509	5	1.0	5	4	US-09-187-859-1905	Sequence 1905, Ap
437	6	1.2	1212	1	US-08-072-574-10	Sequence 10, Appl	510	5	1.0	6	1	US-08-287-717-14	Sequence 14, Appl
438	6	1.2	1212	1	US-08-486-270-10	Sequence 10, Appl	511	5	1.0	6	1	US-08-441-914-14	Sequence 14, Appl
439	6	1.2	1212	3	US-08-367-264-10	Sequence 10, Appl	512	5	1.0	6	2	US-08-340-283-162	Sequence 162, App
440	6	1.2	1212	4	US-08-660-148-5	Sequence 5, Appli	513	5	1.0	6	4	US-09-608-790-5	Sequence 5, Appli
441	6	1.2	1212	4	US-09-153-757-10	Sequence 10, Appl	514	5	1.0	6	4	US-09-608-790-6	Sequence 6, Appli
442	6	1.2	1219	2	US-08-687-289A-6	Sequence 6, Appli	515	5	1.0	7	1	US-08-213-124-3	Sequence 3, Appli
443	6	1.2	1220	2	US-08-843-530B-36	Sequence 36, Appl	516	5	1.0	7	3	US-08-485-324-1	Sequence 1, Appli
444	6	1.2	1227	2	US-08-760-075A-18	Sequence 18, Appl	517	5	1.0	7	3	US-08-485-324-17	Sequence 17, Appl
445	6	1.2	1227	4	US-09-338-546-18	Sequence 18, Appl	518	5	1.0	7	3	US-08-447-506-1	Sequence 1, Appli
446	6	1.2	1227	4	US-09-659-084-18	Sequence 18, Appl	519	5	1.0	7	3	US-08-447-506-17	Sequence 17, Appl
447	6	1.2	1257	4	US-09-220-641-3	Sequence 3, Appli	520	5	1.0	7	3	US-08-235-437-1	Sequence 1, Appli
448	6	1.2	1317	3	US-09-083-521-7	Sequence 7, Appli	521	5	1.0	7	3	US-08-235-437-17	Sequence 17, Appl
449	6	1.2	1326	4	US-09-147-236-5	Sequence 5, Appli	522	5	1.0	7	4	US-09-173-941-102	Sequence 102, App
450	6	1.2	1422	4	US-08-469-260A-85	Sequence 85, Appl	523	5	1.0	7	4	US-08-447-515-1	Sequence 1, Appli
451	6	1.2	1498	2	US-08-404-531B-28	Sequence 28, Appl	524	5	1.0	7	4	US-08-447-515-17	Sequence 17, Appl
452	6	1.2	1498	2	US-08-404-531B-29	Sequence 29, Appl	525	5	1.0	7	4	US-08-469-260A-497	Sequence 497, App
453	6	1.2	1498	3	US-08-476-900A-28	Sequence 28, Appl	526	5	1.0	8	2	US-08-679-865-31	Sequence 31, Appl
454	6	1.2	1498	3	US-08-476-900A-29	Sequence 29, Appl	527	5	1.0	8	2	US-08-679-865-32	Sequence 32, Appl
455	6	1.2	1498	3	US-08-488-546A-28	Sequence 28, Appl	528	5	1.0	8	2	US-08-680-876-31	Sequence 31, Appl
456	6	1.2	1498	3	US-08-488-546A-29	Sequence 29, Appl	529	5	1.0	8	2	US-08-680-876-32	Sequence 32, Appl
457	6	1.2	1536	4	US-09-413-814-10	Sequence 10, Appl	530	5	1.0	8	4	US-09-263-975-31	Sequence 31, Appl
458	6	1.2	1580	4	US-08-726-320-1	Sequence 1, Appli	531	5	1.0	8	4	US-09-263-975-32	Sequence 32, Appl
459	6	1.2	1580	4	US-09-208-716-1	Sequence 1, Appli	532	5	1.0	8	4	US-08-988-842-41	Sequence 41, Appl
460	6	1.2	1581	2	US-08-404-531B-6	Sequence 6, Appli	533	5	1.0	9	1	US-08-465-167A-34	Sequence 34, Appl
461	6	1.2	1581	3	US-08-476-900A-6	Sequence 6, Appli	534	5	1.0	9	2	US-08-640-765A-7	Sequence 7, Appli
462	6	1.2	1581	3	US-08-488-546A-6	Sequence 6, Appli	535	5	1.0	9	2	US-08-340-283-30	Sequence 30, Appl
463	6	1.2	1581	4	US-08-726-320-3	Sequence 3, Appli	536	5	1.0	9	2	US-08-340-283-92	Sequence 92, Appl
464	6	1.2	1581	4	US-08-726-320-4	Sequence 4, Appli	537	5	1.0	9	2	US-08-340-283-114	Sequence 114, App
465	6	1.2	1581	4	US-09-208-716-3	Sequence 3, Appli	538	5	1.0	9	2	US-08-679-865-33	Sequence 33, Appl

539	5	1.0	9	2	US-08-680-876-33	Sequence 33, Appl	612	5	1.0	15	2	US-08-599-654-51	Sequence 51, Appl
540	5	1.0	9	2	US-08-986-234-97	Sequence 97, Appl	613	5	1.0	15	3	US-08-944-868A-51	Sequence 51, Appl
541	5	1.0	9	4	US-09-073-613-7	Sequence 7, Appl	614	5	1.0	15	3	US-08-944-423A-51	Sequence 51, Appl
542	5	1.0	9	4	US-09-263-975-33	Sequence 33, Appl	615	5	1.0	15	3	US-08-466-680B-44	Sequence 44, Appl
543	5	1.0	9	4	US-09-306-542A-39	Sequence 39, Appl	616	5	1.0	15	3	US-08-944-496-51	Sequence 51, Appl
544	5	1.0	9	4	US-09-257-179-112	Sequence 112, App	617	5	1.0	15	4	US-09-230-222-24	Sequence 24, Appl
545	5	1.0	9	4	US-09-359-304B-2	Sequence 2, Appl	618	5	1.0	15	4	US-08-602-999A-366	Sequence 366, App
546	5	1.0	9	4	US-09-359-304B-5	Sequence 5, Appl	619	5	1.0	15	4	US-09-026-904-15	Sequence 15, Appl
547	5	1.0	9	4	US-09-359-304B-7	Sequence 7, Appl	620	5	1.0	15	4	US-09-336-447A-33	Sequence 33, Appl
548	5	1.0	10	1	US-08-075-533-7	Sequence 7, Appl	621	5	1.0	15	4	US-09-009-953-41	Sequence 41, Appl
549	5	1.0	10	1	US-08-465-167A-51	Sequence 51, Appl	622	5	1.0	15	4	US-09-009-953-45	Sequence 45, Appl
550	5	1.0	10	2	US-08-679-865-12	Sequence 12, Appl	623	5	1.0	15	4	US-09-009-953-47	Sequence 47, Appl
551	5	1.0	10	2	US-08-679-865-34	Sequence 34, Appl	624	5	1.0	15	4	US-09-009-953-52	Sequence 52, Appl
552	5	1.0	10	2	US-08-680-876-12	Sequence 12, Appl	625	5	1.0	15	4	US-09-500-124-366	Sequence 366, App
553	5	1.0	10	2	US-08-680-876-34	Sequence 34, Appl	626	5	1.0	15	6	5175148-2	Patent No. 5175148
554	5	1.0	10	2	US-08-948-176-7	Sequence 7, Appl	627	5	1.0	16	3	US-08-912-272-39	Sequence 39, Appl
555	5	1.0	10	3	US-08-159-339A-1038	Sequence 1038, Ap	628	5	1.0	16	4	US-09-323-433A-29	Sequence 29, Appl
556	5	1.0	10	4	US-09-263-975-12	Sequence 12, Appl	629	5	1.0	16	4	US-09-026-039-39	Sequence 39, Appl
557	5	1.0	10	4	US-09-263-975-34	Sequence 34, Appl	630	5	1.0	16	4	US-09-230-225B-7	Sequence 7, Appl
558	5	1.0	10	4	US-09-336-447A-34	Sequence 34, Appl	631	5	1.0	17	2	US-08-319-866-24	Sequence 24, Appl
559	5	1.0	10	5	PCT-US91-09160-7	Sequence 7, Appl	632	5	1.0	17	4	US-09-025-769B-243	Sequence 243, App
560	5	1.0	11	1	US-07-666-719-20	Sequence 20, Appl	633	5	1.0	17	4	US-09-265-653-19	Sequence 19, Appl
561	5	1.0	11	2	US-08-679-865-35	Sequence 35, Appl	634	5	1.0	17	4	US-07-666-719-12	Sequence 12, Appl
562	5	1.0	11	2	US-08-680-876-35	Sequence 35, Appl	635	5	1.0	18	1	US-08-240-514-42	Sequence 42, Appl
563	5	1.0	11	4	US-09-263-975-35	Sequence 35, Appl	636	5	1.0	18	1	US-08-612-302A-42	Sequence 42, Appl
564	5	1.0	12	2	US-08-406-330-80	Sequence 80, Appl	637	5	1.0	18	2	US-09-017-205-41	Sequence 41, Appl
565	5	1.0	12	2	US-08-347-335A-11	Sequence 11, Appl	638	5	1.0	18	2	US-09-017-205-42	Sequence 42, Appl
566	5	1.0	12	2	US-08-556-597-80	Sequence 80, Appl	639	5	1.0	18	3	US-08-912-272-7	Sequence 7, Appl
567	5	1.0	12	3	US-08-599-226-27	Sequence 27, Appl	640	5	1.0	18	3	US-08-912-272-38	Sequence 38, Appl
568	5	1.0	12	3	US-08-599-226-28	Sequence 28, Appl	641	5	1.0	18	3	US-08-912-272-40	Sequence 40, Appl
569	5	1.0	12	3	US-08-599-226-29	Sequence 29, Appl	642	5	1.0	18	4	US-09-157-910-2	Sequence 2, Appl
570	5	1.0	12	3	US-08-599-226-30	Sequence 30, Appl	643	5	1.0	18	4	US-09-026-039-7	Sequence 7, Appl
571	5	1.0	12	3	US-08-599-226-32	Sequence 32, Appl	644	5	1.0	18	4	US-09-026-039-38	Sequence 38, Appl
572	5	1.0	12	3	US-08-599-226-33	Sequence 33, Appl	645	5	1.0	18	4	US-09-026-039-40	Sequence 40, Appl
573	5	1.0	12	4	US-09-125-098-27	Sequence 27, Appl	646	5	1.0	18	4	US-09-082-358B-16	Sequence 16, Appl
574	5	1.0	12	4	US-09-125-098-28	Sequence 28, Appl	647	5	1.0	19	3	US-08-943-173-12	Sequence 12, Appl
575	5	1.0	12	4	US-09-125-098-29	Sequence 29, Appl	648	5	1.0	19	4	US-09-345-468-8	Sequence 8, Appl
576	5	1.0	12	4	US-09-125-098-30	Sequence 30, Appl	649	5	1.0	19	4	US-08-957-130-20	Sequence 20, Appl
577	5	1.0	12	4	US-09-125-098-32	Sequence 32, Appl	650	5	1.0	19	4	US-09-414-453A-8	Sequence 8, Appl
578	5	1.0	12	4	US-09-125-098-33	Sequence 33, Appl	651	5	1.0	19	4	US-08-918-428D-16	Sequence 16, Appl
579	5	1.0	12	4	US-09-025-769B-191	Sequence 191, App	652	5	1.0	20	1	US-07-651-710A-21	Sequence 21, Appl
580	5	1.0	13	1	US-08-075-533-5	Sequence 5, Appl	653	5	1.0	20	1	US-07-798-776-13	Sequence 13, Appl
581	5	1.0	13	2	US-08-292-968-34	Sequence 34, Appl	654	5	1.0	20	1	US-07-798-776-21	Sequence 21, Appl
582	5	1.0	13	2	US-08-679-865-13	Sequence 13, Appl	655	5	1.0	20	1	US-08-218-025A-27	Sequence 27, Appl
583	5	1.0	13	2	US-08-680-876-13	Sequence 13, Appl	656	5	1.0	20	1	US-07-678-974D-8	Sequence 8, Appl
584	5	1.0	13	2	US-08-948-176-5	Sequence 5, Appl	657	5	1.0	20	2	US-08-140-137A-38	Sequence 38, Appl
585	5	1.0	13	2	US-08-467-974-34	Sequence 34, Appl	658	5	1.0	20	2	US-08-934-915-151	Sequence 151, App
586	5	1.0	13	2	US-08-467-976-34	Sequence 34, Appl	659	5	1.0	20	2	US-08-945-168-13	Sequence 13, Appl
587	5	1.0	13	3	US-08-467-976-34	Sequence 34, Appl	660	5	1.0	20	2	US-08-251-288A-13	Sequence 13, Appl
588	5	1.0	13	3	US-08-526-136-21	Sequence 21, Appl	661	5	1.0	20	3	US-08-251-288A-21	Sequence 21, Appl
589	5	1.0	13	4	US-09-082-514-34	Sequence 34, Appl	662	5	1.0	20	3	US-09-298-819A-13	Sequence 13, Appl
590	5	1.0	13	4	US-09-263-975-13	Sequence 13, Appl	663	5	1.0	20	3	US-09-298-819A-21	Sequence 21, Appl
591	5	1.0	13	4	US-08-817-787-7	Sequence 7, Appl	664	5	1.0	20	4	US-09-333-373-1	Sequence 1, Appl
592	5	1.0	13	5	PCT-US91-09160-5	Sequence 5, Appl	665	5	1.0	20	4	US-09-586-563C-13	Sequence 13, Appl
593	5	1.0	14	1	PCT-US95-04121-47	Sequence 47, Appl	666	5	1.0	20	4	US-09-586-563C-21	Sequence 21, Appl
594	5	1.0	14	1	US-08-321-668-24	Sequence 24, Appl	667	5	1.0	20	4	US-09-586-562C-13	Sequence 13, Appl
595	5	1.0	14	1	US-08-837-941-24	Sequence 24, Appl	668	5	1.0	20	4	US-09-586-562C-21	Sequence 21, Appl
596	5	1.0	14	2	US-08-637-759B-153	Sequence 153, App	669	5	1.0	20	6	5427917-1	Patent No. 5427917
597	5	1.0	14	2	US-07-876-941A-23	Sequence 23, Appl	670	5	1.0	21	1	US-07-868-353A-4	Sequence 4, Appl
598	5	1.0	14	3	US-08-871-355A-153	Sequence 153, App	671	5	1.0	21	2	US-08-407-804-4	Sequence 4, Appl
599	5	1.0	14	4	US-09-217-228-17	Sequence 17, Appl	672	5	1.0	21	2	US-08-712-212-2	Sequence 2, Appl
600	5	1.0	14	4	US-09-217-228-18	Sequence 18, Appl	673	5	1.0	21	2	US-08-894-339-8	Sequence 8, Appl
601	5	1.0	14	4	US-09-201-945-153	Sequence 153, App	674	5	1.0	21	3	US-09-124-807-4	Sequence 4, Appl
602	5	1.0	14	4	US-09-400-653A-42	Sequence 42, Appl	675	5	1.0	21	4	US-09-306-044-8	Sequence 8, Appl
603	5	1.0	15	1	US-08-030-731A-27	Sequence 27, Appl	676	5	1.0	21	4	US-09-286-959B-23	Sequence 23, Appl
604	5	1.0	15	1	US-07-854-603-14	Sequence 14, Appl	677	5	1.0	21	4	US-09-106-568E-117	Sequence 117, App
605	5	1.0	15	1	US-08-467-083-44	Sequence 44, Appl	678	5	1.0	21	5	PCT-US95-05160-2	Sequence 2, Appl
606	5	1.0	15	1	US-08-414-417B-44	Sequence 44, Appl	679	5	1.0	22	1	US-08-140-137A-24	Sequence 24, Appl
607	5	1.0	15	2	US-08-140-137A-32	Sequence 32, Appl	680	5	1.0	22	2	US-08-637-759B-114	Sequence 114, App
608	5	1.0	15	2	US-08-486-348A-44	Sequence 44, Appl	681	5	1.0	22	2	US-08-902-516-6	Sequence 6, Appl
609	5	1.0	15	2	US-08-616-844-51	Sequence 51, Appl	682	5	1.0	22	3	US-08-871-355A-114	Sequence 114, App
610	5	1.0	15	2	US-08-687-956A-9	Sequence 9, Appl	683	5	1.0	22	4	US-09-201-945-114	Sequence 114, App
611	5	1.0	15	2	US-08-468-545B-44	Sequence 44, Appl	684	5	1.0	22	4	US-09-106-568E-29	Sequence 29, Appl

685	5	1.0	22	4	US-09-106-568E-69	Sequence 69, Appl	758	5	1.0	29	4	US-09-699-684-12	Sequence 12, Appl
686	5	1.0	22	6	5266328-12	Patent No. 5266328	759	5	1.0	29	4	US-09-699-684-20	Sequence 20, Appl
687	5	1.0	23	1	US-07-908-317-11	Sequence 11, Appl	760	5	1.0	29	6	5204096-34	Patent No. 5204096
688	5	1.0	23	1	US-08-264-093-23	Sequence 23, Appl	761	5	1.0	30	1	US-08-084-741A-5	Sequence 5, Appl
689	5	1.0	23	1	US-08-112-208C-17	Sequence 17, Appl	762	5	1.0	30	1	US-08-184-252A-7	Sequence 7, Appl
690	5	1.0	23	1	US-08-248-819A-19	Sequence 19, Appl	763	5	1.0	30	2	US-08-140-137A-41	Sequence 41, Appl
691	5	1.0	23	2	US-08-630-822A-75	Sequence 75, Appl	764	5	1.0	30	2	US-08-318-157B-30	Sequence 30, Appl
692	5	1.0	23	2	US-08-337-646A-37	Sequence 37, Appl	765	5	1.0	30	2	US-08-318-157B-32	Sequence 32, Appl
693	5	1.0	23	2	US-09-005-069-75	Sequence 75, Appl	766	5	1.0	30	4	US-09-348-578-5	Sequence 5, Appl
694	5	1.0	23	2	US-08-856-531-17	Sequence 17, Appl	767	5	1.0	30	4	US-09-348-578-13	Sequence 13, Appl
695	5	1.0	23	2	US-08-856-034-17	Sequence 17, Appl	768	5	1.0	30	4	US-09-348-578-21	Sequence 21, Appl
696	5	1.0	23	4	US-08-927-326-23	Sequence 23, Appl	769	5	1.0	30	4	US-09-699-684-5	Sequence 5, Appl
697	5	1.0	23	4	US-08-927-326-37	Sequence 37, Appl	770	5	1.0	30	4	US-09-699-684-13	Sequence 13, Appl
698	5	1.0	23	4	US-09-171-156A-4	Sequence 4, Appl	771	5	1.0	30	5	PCT-US95-00601-7	Sequence 7, Appl
699	5	1.0	23	4	US-09-186-276B-8	Sequence 8, Appl	772	5	1.0	30	5	PCT-US95-00601-7	Sequence 7, Appl
700	5	1.0	23	4	US-09-186-276B-8	Sequence 8, Appl	773	5	1.0	30	6	5464764-1	Patent No. 5464764
701	5	1.0	23	4	US-09-149-476-328	Sequence 328, App	774	5	1.0	31	1	US-08-190-802A-239	Sequence 239, App
702	5	1.0	23	4	US-08-842-445-5	Sequence 5, Appl	775	5	1.0	31	3	US-07-401-432-31	Sequence 31, Appl
703	5	1.0	23	4	US-08-842-445-5	Sequence 5, Appl	776	5	1.0	31	3	US-07-401-432-32	Sequence 32, Appl
704	5	1.0	23	4	US-09-186-188B-5	Sequence 5, Appl	777	5	1.0	31	4	US-09-348-578-6	Sequence 6, Appl
705	5	1.0	23	4	US-09-186-188B-8	Sequence 8, Appl	778	5	1.0	31	4	US-09-348-578-14	Sequence 14, Appl
706	5	1.0	23	4	PCT-US93-06171-11	Sequence 11, Appl	779	5	1.0	31	4	US-09-348-578-22	Sequence 22, Appl
707	5	1.0	23	5	PCT-US93-06171-11	Sequence 11, Appl	780	5	1.0	31	4	US-08-477-346-239	Sequence 239, App
708	5	1.0	24	1	US-07-794-288D-189	Sequence 189, App	781	5	1.0	31	4	US-08-473-089-239	Sequence 239, App
709	5	1.0	24	2	US-08-140-137A-37	Sequence 37, Appl	782	5	1.0	31	4	US-08-487-072A-239	Sequence 239, App
710	5	1.0	24	2	US-08-347-335A-19	Sequence 19, Appl	783	5	1.0	31	4	US-09-699-684-6	Sequence 6, Appl
711	5	1.0	24	2	US-09-000-041A-13	Sequence 13, Appl	784	5	1.0	31	4	US-09-699-684-14	Sequence 14, Appl
712	5	1.0	24	5	PCT-US92-07865-16	Sequence 16, Appl	785	5	1.0	31	4	US-09-699-684-22	Sequence 22, Appl
713	5	1.0	25	1	US-07-794-288D-181	Sequence 181, App	786	5	1.0	31	6	5245013-18	Patent No. 5245013
714	5	1.0	25	2	US-08-337-646A-29	Sequence 29, Appl	787	5	1.0	32	1	US-07-995-503A-5	Sequence 5, Appl
715	5	1.0	25	2	US-08-726-306A-67	Sequence 67, Appl	788	5	1.0	32	1	US-08-390-510-5	Sequence 5, Appl
716	5	1.0	25	4	US-08-927-326-29	Sequence 29, Appl	789	5	1.0	32	1	US-08-390-510-5	Sequence 5, Appl
717	5	1.0	25	4	US-09-336-536-52	Sequence 52, Appl	790	5	1.0	32	2	US-08-140-137A-27	Sequence 27, Appl
718	5	1.0	25	4	US-09-149-476-369	Sequence 369, App	791	5	1.0	32	2	US-08-390-509-5	Sequence 5, Appl
719	5	1.0	25	4	US-08-469-260A-180	Sequence 180, App	792	5	1.0	32	2	US-08-526-583-14	Sequence 14, Appl
720	5	1.0	26	4	US-08-918-428D-13	Sequence 13, Appl	793	5	1.0	32	2	US-08-595-868C-39	Sequence 39, Appl
721	5	1.0	26	4	US-09-082-358B-83	Sequence 83, Appl	794	5	1.0	32	2	US-08-595-868C-40	Sequence 40, Appl
722	5	1.0	27	1	US-08-140-188-13	Sequence 13, Appl	795	5	1.0	32	4	US-09-348-578-7	Sequence 7, Appl
723	5	1.0	27	1	US-08-481-888A-2	Sequence 2, Appl	796	5	1.0	32	4	US-09-348-578-15	Sequence 15, Appl
724	5	1.0	27	1	US-08-485-273A-2	Sequence 2, Appl	797	5	1.0	32	4	US-09-348-578-23	Sequence 23, Appl
725	5	1.0	27	2	US-08-522-229B-3	Sequence 3, Appl	798	5	1.0	32	4	US-09-149-860A-5	Sequence 5, Appl
726	5	1.0	27	2	US-08-169-948B-22	Sequence 22, Appl	799	5	1.0	32	4	US-09-139-819A-39	Sequence 39, Appl
727	5	1.0	27	2	US-08-448-873-22	Sequence 22, Appl	800	5	1.0	32	4	US-09-139-819A-40	Sequence 40, Appl
728	5	1.0	27	2	US-09-102-433-3	Sequence 3, Appl	801	5	1.0	32	4	US-09-227-357-181	Sequence 181, App
729	5	1.0	27	2	US-08-973-563A-2	Sequence 2, Appl	802	5	1.0	32	4	US-08-936-165A-459	Sequence 459, App
730	5	1.0	27	2	US-08-973-559-2	Sequence 2, Appl	803	5	1.0	32	4	US-09-750-913-39	Sequence 39, Appl
731	5	1.0	27	3	US-08-526-521-13	Sequence 13, Appl	804	5	1.0	32	4	US-09-750-913-40	Sequence 40, Appl
732	5	1.0	27	3	US-08-749-816-19	Sequence 19, Appl	805	5	1.0	32	4	US-09-699-684-7	Sequence 7, Appl
733	5	1.0	27	4	US-09-348-578-2	Sequence 2, Appl	806	5	1.0	32	4	US-09-699-684-15	Sequence 15, Appl
734	5	1.0	27	4	US-09-345-468-21	Sequence 21, Appl	807	5	1.0	32	4	US-09-699-684-23	Sequence 23, Appl
735	5	1.0	27	4	US-08-382-452D-22	Sequence 22, Appl	808	5	1.0	32	4	US-08-737-109-22	Sequence 22, Appl
736	5	1.0	27	4	US-09-144-914-23	Sequence 23, Appl	809	5	1.0	32	4	US-09-082-358B-40	Sequence 40, Appl
737	5	1.0	27	4	US-09-227-357-291	Sequence 291, App	810	5	1.0	33	4	US-09-348-578-8	Sequence 8, Appl
738	5	1.0	27	4	US-09-414-453A-21	Sequence 21, Appl	811	5	1.0	33	4	US-09-348-578-16	Sequence 16, Appl
739	5	1.0	27	4	US-09-699-684-2	Sequence 2, Appl	812	5	1.0	33	4	US-09-348-578-24	Sequence 24, Appl
740	5	1.0	27	4	US-08-469-260A-481	Sequence 481, App	813	5	1.0	33	4	US-09-699-684-8	Sequence 8, Appl
741	5	1.0	28	1	US-08-105-483-445	Sequence 445, App	814	5	1.0	33	4	US-09-699-684-16	Sequence 16, Appl
742	5	1.0	28	1	US-08-709-209-445	Sequence 445, App	815	5	1.0	33	4	US-09-699-684-24	Sequence 24, Appl
743	5	1.0	28	1	US-08-303-275-156	Sequence 156, App	816	5	1.0	34	2	US-08-445-520B-3	Sequence 3, Appl
744	5	1.0	28	1	US-08-458-101-445	Sequence 445, App	817	5	1.0	34	3	US-08-658-136-38	Sequence 38, Appl
745	5	1.0	28	4	US-09-348-578-3	Sequence 3, Appl	818	5	1.0	34	4	US-09-348-578-9	Sequence 9, Appl
746	5	1.0	28	4	US-09-348-578-11	Sequence 11, Appl	819	5	1.0	34	4	US-09-348-578-17	Sequence 17, Appl
747	5	1.0	28	4	US-09-364-946-5	Sequence 5, Appl	820	5	1.0	34	4	US-09-348-578-25	Sequence 25, Appl
748	5	1.0	28	4	US-09-364-946-9	Sequence 9, Appl	821	5	1.0	34	4	US-09-239-864A-3	Sequence 3, Appl
749	5	1.0	28	4	US-09-699-684-3	Sequence 3, Appl	822	5	1.0	34	4	US-09-227-357-606	Sequence 606, App
750	5	1.0	28	4	US-09-699-684-11	Sequence 11, Appl	823	5	1.0	34	4	US-09-301-978C-24	Sequence 24, Appl
751	5	1.0	29	2	US-08-708-856A-5	Sequence 5, Appl	824	5	1.0	34	4	US-09-699-684-9	Sequence 9, Appl
752	5	1.0	29	3	US-09-287-375-5	Sequence 5, Appl	825	5	1.0	34	4	US-09-699-684-17	Sequence 17, Appl
753	5	1.0	29	4	US-09-348-578-4	Sequence 4, Appl	826	5	1.0	34	4	US-09-699-684-25	Sequence 25, Appl
754	5	1.0	29	4	US-09-348-578-12	Sequence 12, Appl	827	5	1.0	35	2	US-08-140-137A-45	Sequence 45, Appl
755	5	1.0	29	4	US-09-348-578-20	Sequence 20, Appl	828	5	1.0	35	4	US-09-348-578-18	Sequence 18, Appl
756	5	1.0	29	4	US-09-455-406-5	Sequence 5, Appl	829	5	1.0	35	4	US-09-348-578-26	Sequence 26, Appl
757	5	1.0	29	4	US-09-699-684-4	Sequence 4, Appl	830	5	1.0	35	4	US-09-082-279B-636	Sequence 636, App

831	5	1.0	35	4	US-09-315-304B-636	Sequence 636, App	904	5	1.0	47	3	US-09-100-600A-76	Sequence 76, Appl
832	5	1.0	35	4	US-08-857-046A-19	Sequence 19, Appl	905	5	1.0	47	3	US-09-100-600A-81	Sequence 81, Appl
833	5	1.0	35	4	US-09-699-684-18	Sequence 18, Appl	906	5	1.0	47	3	US-09-100-600A-82	Sequence 82, Appl
834	5	1.0	35	4	US-09-699-684-26	Sequence 26, Appl	907	5	1.0	47	3	US-09-100-600A-84	Sequence 84, Appl
835	5	1.0	35	4	US-08-411-098-15	Sequence 15, Appl	908	5	1.0	47	3	US-09-100-600A-85	Sequence 85, Appl
836	5	1.0	36	2	US-08-411-098-15	Sequence 27, Appl	909	5	1.0	47	3	US-09-100-600A-86	Sequence 86, Appl
837	5	1.0	36	4	US-09-348-578-27	Sequence 27, Appl	910	5	1.0	47	4	US-08-477-346-186	Sequence 186, App
838	5	1.0	37	4	US-09-699-684-27	Sequence 3, Appli	911	5	1.0	47	4	US-08-477-346-186	Sequence 186, App
839	5	1.0	37	4	US-08-817-787-30	Sequence 10, Appl	912	5	1.0	47	4	US-09-257-179-65	Sequence 65, Appl
840	5	1.0	38	1	US-08-287-717-9	Sequence 9, Appli	913	5	1.0	47	4	US-09-149-476-435	Sequence 435, App
841	5	1.0	38	1	US-08-176-500-2	Sequence 2, Appli	914	5	1.0	47	4	US-08-487-072A-186	Sequence 186, App
842	5	1.0	38	1	US-08-176-500-127	Sequence 127, App	915	5	1.0	48	1	US-08-485-455D-65	Sequence 65, App
843	5	1.0	38	1	US-08-471-052A-2	Sequence 2, Appli	916	5	1.0	48	1	US-08-482-130C-65	Sequence 65, Appl
844	5	1.0	38	1	US-08-471-052A-127	Sequence 127, App	917	5	1.0	48	2	US-08-484-211C-65	Sequence 65, Appl
845	5	1.0	38	1	US-08-481-888A-1	Sequence 1, Appli	918	5	1.0	48	2	US-08-906-769-65	Sequence 65, Appl
846	5	1.0	38	1	US-08-485-273A-1	Sequence 1, Appli	919	5	1.0	48	3	US-08-906-769-65	Sequence 65, Appl
847	5	1.0	38	1	US-08-441-914-9	Sequence 9, Appli	920	5	1.0	48	4	US-08-817-795-65	Sequence 65, Appl
848	5	1.0	38	1	US-08-189-331-2	Sequence 2, Appli	921	5	1.0	48	4	US-08-448-619-8	Sequence 8, Appli
849	5	1.0	38	1	US-08-189-331-127	Sequence 127, App	922	5	1.0	48	4	US-08-448-619-9	Sequence 9, Appli
850	5	1.0	38	1	US-08-324-977-30	Sequence 30, Appl	923	5	1.0	48	4	US-08-485-443B-65	Sequence 65, Appl
851	5	1.0	38	2	US-08-471-939-2	Sequence 2, Appli	924	5	1.0	48	4	US-08-639-075A-65	Sequence 65, Appl
852	5	1.0	38	2	US-08-471-939-127	Sequence 127, App	925	5	1.0	48	4	US-09-012-431-65	Sequence 65, Appl
853	5	1.0	38	2	US-08-384-616-30	Sequence 30, Appl	926	5	1.0	48	4	US-09-012-431-65	Sequence 65, Appl
854	5	1.0	38	2	US-08-471-800-2	Sequence 2, Appli	927	5	1.0	48	4	US-08-906-613-65	Sequence 65, Appl
855	5	1.0	38	2	US-08-471-800-127	Sequence 127, App	928	5	1.0	48	4	US-08-936-165A-530	Sequence 530, App
856	5	1.0	38	2	US-08-973-563A-1	Sequence 1, Appli	929	5	1.0	48	4	US-09-288-143-212	Sequence 212, App
857	5	1.0	38	2	US-08-973-559-1	Sequence 1, Appli	930	5	1.0	48	5	PCT-US95-144A2A-65	Sequence 65, Appl
858	5	1.0	38	2	US-08-471-068-2	Sequence 2, Appli	931	5	1.0	49	3	US-08-919-597-239	Sequence 239, App
859	5	1.0	38	2	US-08-471-068-127	Sequence 127, App	932	5	1.0	49	3	US-09-217-228-9	Sequence 9, Appli
860	5	1.0	38	2	US-08-904-686A-30	Sequence 30, Appl	933	5	1.0	50	2	US-08-980-071-37	Sequence 37, Appl
861	5	1.0	38	3	US-08-808-130-4	Sequence 4, Appli	934	5	1.0	50	2	US-08-757-536-37	Sequence 37, Appl
862	5	1.0	38	3	US-08-808-130-5	Sequence 5, Appli	935	5	1.0	50	3	US-08-468-011A-13	Sequence 13, Appl
863	5	1.0	38	3	US-08-491-954-37	Sequence 37, Appl	936	5	1.0	50	3	US-09-314-093-37	Sequence 37, Appl
864	5	1.0	38	4	US-09-315-850-30	Sequence 30, Appl	937	5	1.0	50	4	US-09-250-848-37	Sequence 37, Appl
865	5	1.0	38	4	US-09-202-316-3	Sequence 3, Appli	938	5	1.0	50	4	US-09-251-885-37	Sequence 37, Appl
866	5	1.0	39	1	US-07-666-719-5	Sequence 5, Appli	939	5	1.0	50	4	US-09-007-905-26	Sequence 26, Appl
867	5	1.0	39	1	US-08-189-331-143	Sequence 143, App	940	5	1.0	50	4	US-09-232-074-26	Sequence 27, Appl
868	5	1.0	39	2	US-08-471-068-143	Sequence 3, Appli	941	5	1.0	50	4	US-09-337-280-37	Sequence 37, Appl
869	5	1.0	40	1	US-08-735-963-3	Sequence 3, Appli	942	5	1.0	50	4	US-08-570-157-8	Sequence 8, Appli
870	5	1.0	40	2	US-09-105-057-3	Sequence 32, Appl	943	5	1.0	51	1	US-08-570-157-9	Sequence 9, Appli
871	5	1.0	40	2	US-08-807-332B-32	Sequence 32, Appl	944	5	1.0	51	1	US-08-570-157-10	Sequence 10, Appl
872	5	1.0	40	4	US-09-338-876-32	Sequence 32, Appl	945	5	1.0	51	1	US-08-570-157-11	Sequence 11, Appl
873	5	1.0	40	4	US-09-304-214-3	Sequence 3, Appli	946	5	1.0	51	1	US-08-570-157-12	Sequence 12, Appl
874	5	1.0	41	4	US-09-007-905-70	Sequence 70, Appl	947	5	1.0	51	1	US-08-570-157-15	Sequence 15, Appl
875	5	1.0	41	4	US-09-232-074-70	Sequence 70, Appl	948	5	1.0	51	1	US-08-570-157-16	Sequence 16, Appl
876	5	1.0	42	1	US-07-651-710A-25	Sequence 25, Appl	949	5	1.0	51	1	US-08-570-157-17	Sequence 17, Appl
877	5	1.0	43	1	US-08-078-683A-10	Sequence 10, Appl	950	5	1.0	51	1	US-08-570-157-18	Sequence 18, Appl
878	5	1.0	43	3	US-08-946-026-5	Sequence 5, Appli	951	5	1.0	51	1	US-08-570-157-19	Sequence 19, Appl
879	5	1.0	43	4	US-09-502-653-5	Sequence 5, Appli	952	5	1.0	51	1	US-08-570-157-20	Sequence 20, Appl
880	5	1.0	43	4	US-09-445-247-16	Sequence 16, Appl	953	5	1.0	51	1	US-08-570-157-21	Sequence 21, Appl
881	5	1.0	44	1	US-08-208-008C-6	Sequence 6, Appli	954	5	1.0	51	1	US-08-570-157-22	Sequence 22, Appl
882	5	1.0	44	2	US-08-140-137A-48	Sequence 48, Appl	955	5	1.0	51	1	US-08-570-157-23	Sequence 23, Appl
883	5	1.0	44	3	US-09-053-197A-56	Sequence 56, Appl	956	5	1.0	51	3	US-08-974-022-44	Sequence 44, Appl
884	5	1.0	44	4	US-08-085-761A-61	Sequence 61, Appl	957	5	1.0	51	4	US-08-795-447A-44	Sequence 44, Appl
885	5	1.0	45	2	US-08-530-290-21	Sequence 21, Appl	958	5	1.0	51	4	US-08-795-447A-44	Sequence 44, Appl
886	5	1.0	45	4	US-08-346-860-5	Sequence 5, Appli	959	5	1.0	51	4	US-08-795-446B-44	Sequence 44, Appl
887	5	1.0	45	4	US-08-857-076-69	Sequence 69, Appl	960	5	1.0	51	4	US-08-795-446B-44	Sequence 44, Appl
888	5	1.0	45	4	US-08-963-851-10	Sequence 10, Appl	961	5	1.0	51	4	US-09-655-270A-35	Sequence 35, Appl
889	5	1.0	45	4	US-09-288-143-82	Sequence 82, Appl	962	5	1.0	51	4	US-08-706-945D-144	Sequence 144, App
890	5	1.0	45	4	US-09-082-358B-79	Sequence 79, Appl	963	5	1.0	51	4	US-09-076-510-8	Sequence 8, Appli
891	5	1.0	46	1	US-08-466-127-7	Sequence 7, Appli	964	5	1.0	51	4	US-09-076-510-9	Sequence 9, Appli
892	5	1.0	46	2	US-08-639-857-30	Sequence 30, App	965	5	1.0	51	4	US-09-076-510-10	Sequence 10, Appl
893	5	1.0	46	2	US-08-726-306A-110	Sequence 110, App	966	5	1.0	51	4	US-09-076-510-11	Sequence 11, Appl
894	5	1.0	46	2	US-08-726-306A-115	Sequence 115, App	967	5	1.0	51	4	US-09-076-510-12	Sequence 12, Appl
895	5	1.0	46	2	US-08-726-306A-177	Sequence 177, App	968	5	1.0	51	4	US-09-076-510-15	Sequence 15, Appl
896	5	1.0	46	3	US-08-955-937A-10	Sequence 10, Appl	969	5	1.0	51	4	US-09-076-510-16	Sequence 16, Appl
897	5	1.0	46	3	US-08-822-324-9	Sequence 9, Appli	970	5	1.0	51	4	US-09-076-510-17	Sequence 17, Appl
898	5	1.0	46	4	US-09-300-985-10	Sequence 10, Appl	971	5	1.0	51	4	US-09-076-510-18	Sequence 18, Appl
899	5	1.0	46	4	US-09-384-302A-29	Sequence 29, Appl	972	5	1.0	51	4	US-09-076-510-19	Sequence 19, Appl
900	5	1.0	47	1	US-08-190-802A-186	Sequence 186, App	973	5	1.0	51	4	US-09-076-510-20	Sequence 20, Appl
901	5	1.0	47	1	US-08-415-751-12	Sequence 12, Appl	974	5	1.0	51	4	US-09-076-510-21	Sequence 21, Appl
902	5	1.0	47	3	US-09-100-600A-71	Sequence 71, Appl	975	5	1.0	51	4	US-09-076-510-22	Sequence 22, Appl
903	5	1.0	47	3	US-09-100-600A-72	Sequence 72, Appl	976	5	1.0	51	4		

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977      5      1.0      51      4      US-09-076-510-23      Sequence 23, Appl
978      5      1.0      52      1      US-08-361-920-17      Sequence 17, Appl
979      5      1.0      52      1      US-08-159-340A-7      Sequence 7, Appl
980      5      1.0      52      1      US-08-479-939-17      Sequence 17, Appl
981      5      1.0      52      1      US-08-483-432-17      Sequence 17, Appl
982      5      1.0      52      3      US-08-906-769-85      Sequence 85, Appl
983      5      1.0      52      3      US-08-906-616-85      Sequence 85, Appl
984      5      1.0      52      4      US-08-817-795-85      Sequence 85, Appl
985      5      1.0      52      4      US-08-639-075A-85      Sequence 85, Appl
986      5      1.0      52      4      US-09-012-431-85      Sequence 85, Appl
987      5      1.0      52      4      US-08-927-219-45      Sequence 45, Appl
988      5      1.0      52      4      US-08-569-749-11      Sequence 11, Appl
989      5      1.0      52      4      US-08-569-749-12      Sequence 12, Appl
990      5      1.0      52      4      US-09-012-692-85      Sequence 85, Appl
991      5      1.0      52      4      US-08-906-613-85      Sequence 13, Appl
992      5      1.0      52      4      US-09-236-468A-13      Sequence 13, Appl
993      5      1.0      52      4      US-09-149-476-632      Sequence 632, App
994      5      1.0      52      5      PCT-US95-14442A-85      Sequence 85, Appl
995      5      1.0      52      5      PCT-US96-12860-11      Sequence 11, Appl
996      5      1.0      52      5      PCT-US96-12860-12      Sequence 12, Appl
997      5      1.0      54      2      US-08-319-866-3      Sequence 3, Appl
998      5      1.0      54      2      US-08-319-866-4      Sequence 4, Appl
999      5      1.0      54      2      US-08-319-866-5      Sequence 5, Appl
1000     5      1.0      54      2      US-08-319-866-6      Sequence 6, Appl

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ALIGNMENTS

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RESULT 1
US-08-564-972-22
; Sequence 22, Application US/08564972
; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Contl-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-564-972-22

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Query Match      1.4%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

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QY 132 ASRVVLS 138
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Db 11 ASRVVLS 17

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RESULT 2

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US-08-564-972-23
; Sequence 23, Application US/08564972
; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Contl-Fine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-564-972-23

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Query Match      1.4%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

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QY 132 ASRVVLS 138
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Db 1 ASRVVLS 7

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RESULT 3

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US-09-152-060-74
; Sequence 74, Application US/09152060

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; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (71)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-74

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Query Match 1.4%; Score 7; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 42 RGNRRA 48
DB 33 RGNRRA 39

RESULT 4
US-08-564-972-8
; Sequence 8, Application US/08564972
; Patent No. 5843462
; GENERAL INFORMATION:
; APPLICANT: Contifine, B. M.
; TITLE OF INVENTION: DIPHTHERIA TOXIM EPITOPES
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
; STREET: P.O. Box 2938
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/564,972
; FILING DATE: 30-NOV-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 600.344US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-564-972-8

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Query Match 1.4%; Score 7; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 132 ASRVVLS 138
DB 131 ASRVVLS 137

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RESULT 5
US-08-148-058A-27
; Sequence 27, Application US/08148058A
; Patent No. 5804407
; GENERAL INFORMATION:
; APPLICANT: TAMAOKI, TAIKI
; APPLICANT: NAKABAYASHI, HIDEKAZU
; TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
; TITLE OF INVENTION: MAMMALIAN CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 PRINCE STREET
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,058A
; FILING DATE: 04-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOL, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-148-058A-27
    Query Match 1.4%; Score 7; DB 1; Length 194;
    Best Local Similarity 100.0%; Pred. No. 40;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 ASRVVLS 138
    |||||
Db 132 ASRVVLS 138

RESULT 6
US-08-148-058A-29
; Sequence 29, Application US/08148058A
; Patent No. 5804407
; GENERAL INFORMATION:
; APPLICANT: TAMAOKI, TAIKI
; APPLICANT: NAKABAYASHI, HIDEKAZU
; TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
; TITLE OF INVENTION: MAMMALIAN CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 PRINCE STREET
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,058A
; FILING DATE: 04-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-148-058A-29
    Query Match 1.4%; Score 7; DB 1; Length 194;
    Best Local Similarity 100.0%; Pred. No. 40;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 ASRVVLS 138
    |||||
Db 132 ASRVVLS 138

RESULT 7
US-08-478-042-27
; Sequence 27, Application US/08478042
; Patent No. 5807738
; GENERAL INFORMATION:
; APPLICANT: TAMAOKI, TAIKI
; APPLICANT: NAKABAYASHI, HIDEKAZU
; TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
; TITLE OF INVENTION: MAMMALIAN CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 PRINCE STREET
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,042
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/148,058
; FILING DATE: 04-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-042-27
    Query Match 1.4%; Score 7; DB 1; Length 194;
    Best Local Similarity 100.0%; Pred. No. 40;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 ASRVVLS 138
    |||||
Db 132 ASRVVLS 138

RESULT 8
US-08-478-042-29
; Sequence 29, Application US/08478042
; Patent No. 5807738
; GENERAL INFORMATION:
; APPLICANT: TAMAOKI, TAIKI
; APPLICANT: NAKABAYASHI, HIDEKAZU
; TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
; TITLE OF INVENTION: MAMMALIAN CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 PRINCE STREET
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,042
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/148,058
; FILING DATE: 04-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-042-29
    Query Match 1.4%; Score 7; DB 1; Length 194;
    Best Local Similarity 100.0%; Pred. No. 40;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 ASRVVLS 138
    |||||
Db 132 ASRVVLS 138

```


NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-478-042-29

Query Match 1.4%; Score 7; DB 1; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVVLS 138
|||||
Db 132 ASRVVLS 138

RESULT 9
US-08-645-215-27
Sequence 27, Application US/08645215
Patent No. 5827686
GENERAL INFORMATION:
APPLICANT: TAMAOKI, TAIKI
APPLICANT: NAKABAYASHI, HIDEKAZU
TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 699 PRINCE STREET
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,215
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,058
FILING DATE: 04-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-135
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-645-215-27

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVVLS 138
|||||

Db 132 ASRVVLS 138

RESULT 10
US-08-645-215-29
Sequence 29, Application US/08645215
Patent No. 5827686
GENERAL INFORMATION:
APPLICANT: TAMAOKI, TAIKI
APPLICANT: NAKABAYASHI, HIDEKAZU
TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 699 PRINCE STREET
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,215
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,058
FILING DATE: 04-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-135
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-645-215-29

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVVLS 138
|||||
Db 132 ASRVVLS 138

RESULT 11
US-08-466-604-27
Sequence 27, Application US/08466604
Patent No. 5843776
GENERAL INFORMATION:
APPLICANT: TAMAOKI, TAIKI
APPLICANT: NAKABAYASHI, HIDEKAZU
TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 PRINCE STREET
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,604
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,058
; FILING DATE: 04-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-466-604-27

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVVLS 138
Db 132 ASRVVLS 138
|||||

RESULT 13
US-09-198-603C-8
; Sequence 8, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
; APPLICANT: TULLY, Raymond E.
; APPLICANT: CALTAGIRONE, G. Thomas
; APPLICANT: MOYER, Shawn S.
; APPLICANT: RONNING, Michael T.
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
; FILE REFERENCE: A7290
; CURRENT APPLICATION NUMBER: US/09/198,603C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Human
US-09-198-603C-8

Query Match 1.4%; Score 7; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 SRLYGPS 100
Db 132 SRLYGPS 138
|||||

RESULT 14
US-09-306-595C-8
; Sequence 8, Application US/09306595C
; Patent No. 6284506
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ISOPRENOID PRODUCTION
; FILE REFERENCE: ISOPRENOID PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/306,595C
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 98108210
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-306-595C-8

Query Match 1.4%; Score 7; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,604
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,058
; FILING DATE: 04-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-466-604-29

Query Match 1.4%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 ASRVVLS 138
Db 132 ASRVVLS 138
|||||

RESULT 12
US-08-466-604-29
; Sequence 29, Application US/08466604
; Patent No. 5843776
; GENERAL INFORMATION:
; APPLICANT: TAMAOKI, TAIKI
; APPLICANT: NAKAYASHI, HIDEKAZU
; TITLE OF INVENTION: IMPROVED METHOD OF EXPRESSING GENES IN
; TITLE OF INVENTION: MAMMALIAN CELLS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 PRINCE STREET
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,604
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,058
; FILING DATE: 04-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 29:
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Qy 381 TTTSSSL 387
 |||||
 Db 45 TTTSSSL 51

RESULT 15

US-08-203-905B-2
 ; Sequence 2, Application US/08203905B
 ; Patent No. 5646249
 ; GENERAL INFORMATION:
 ; APPLICANT: KAYE, FEDERIC J.
 ; APPLICANT: OTTERSON, GREGORY A.
 ; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A
 ; TITLE OF INVENTION: NOVEL CHAPERONE PROTEIN
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
 ; STREET: 620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR
 ; CITY: NEWPORT BEACH
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/08/203.905B
 ; APPLICATION NUMBER: US/08/203.905B
 ; FILING DATE: February 28, 1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KIRKPATRICK, ANITA M.
 ; REGISTRATION NUMBER: 32,617
 ; REFERENCE/DOCKET NUMBER: NIH089.001A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8550
 ; TELEFAX: 619-235-0176
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 471 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-203-905B-2

Query Match 1.48; Score 7; DB 1; Length 471;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 DLGGGTL 72
 |||||
 Db 225 DLGGGTL 231

Search completed: April 22, 2003, 16:20:12
 Job time : 50 secs

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	2185	81.2	431	9	US-09-912-935-36	Sequence 36, Appl
2	1295	48.1	499	9	US-09-912-935-31	Sequence 31, Appl
3	1295	48.1	529	9	US-09-912-935-28	Sequence 28, Appl
4	1295	48.1	529	9	US-09-912-935-40	Sequence 40, Appl
5	1294	48.1	529	9	US-10-066-550-138	Sequence 128, App
6	1294	48.1	529	9	US-10-174-590-472	Sequence 472, App
7	1294	48.1	529	9	US-10-176-758-472	Sequence 472, App
8	1294	48.1	529	9	US-10-175-737-472	Sequence 472, App
9	1294	48.1	529	9	US-10-173-706-472	Sequence 472, App
10	1294	48.1	529	9	US-10-175-738-472	Sequence 472, App
11	1294	48.1	529	9	US-10-175-752-472	Sequence 472, App
12	1294	48.1	529	9	US-10-176-483-472	Sequence 472, App
13	1294	48.1	529	9	US-10-176-757-472	Sequence 472, App
14	1294	48.1	529	9	US-10-176-913-472	Sequence 472, App
15	1294	48.1	529	9	US-10-180-552-472	Sequence 472, App
16	1294	48.1	529	9	US-10-180-557-472	Sequence 472, App
17	1294	48.1	529	9	US-10-173-700-472	Sequence 472, App
18	1294	48.1	529	9	US-10-174-572-472	Sequence 472, App
19	1294	48.1	529	9	US-10-174-579-472	Sequence 472, App

Db 241 ACMSSDLTFNCWCHVLRQCSGSDRYRQWMDGTGCAQAEAG-----QDVRLGPGMRT 294
Qy 364 HDSASPDTSFSPYDGLTSSSLFIDSLTDDTKLNPYAGDGLONNLSPKTKGTPVH 423
Db 295 TTSASPDTSFSPYDGLTSSSLFIDSLTDDTKLNPYAGDGLONNLSPKTKGTPVH 354
Qy 424 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAE 483
Db 355 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAE 414
Qy 484 VEPSGHEKEGMEABQC 500
Db 415 VEPSGHEKEGMEABQC 431

RESULT 2

US-09-912-935-31
; Sequence 31, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912.935
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-31

Query Match 48.1%; Score 1295; DB 9; Length 499;
Best Local Similarity 57.3%; Pred. No. 2.1e-108;
Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;

Qy 72 LAMDTLPDNRTRVVED-NHSYVVSRLYGPSPHSELRVWDVAEANRSOVKIHTILSNTHR 130
Db 65 LLLDDGQDNNTQIEEDTDHNYIISRIYGPSDSASRDLWNIDQMEKDKVKIHGILSNTHR 124
Qy 131 QASRVVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPYSDNS 190
Db 125 QAARVNLSDFAFVVVHRIQIIPNVRRTIYEHVRLMATAQYIAPLMANFNPYSDNS 184
Qy 191 TVVYFDNGTVFVQWQDHVYLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 185 TVRYFDNGTALVQWQDHVYLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 244
Qy 251 PVKGLSDAFVNLNPSDPVPSRRSIFRYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 310
Db 245 PVKGLSDAFVNLNPSDPVPSRRSIFRYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 304
Qy 311 DACMSSDLTFNCWCHVLRQCSGSDRYRQWMDGTGCAQAEAGRMCEDFODEDHDSASPD 370
Db 305 GPCVSSQIGFNCWCHVLRQCSGSDRYRQWMDGTGCAQAEAGRMCEDFODEDHDSASPD 364
Qy 371 T--SFSPYDGLTSSS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 365 TIGATTQFRVLTTRRAVTSQFTSLPTEDDTKIALHLKDNASTDDSAEKKGGTLHA 424
Qy 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAEV 484
Db 425 GLVIGLILVILVATAILVTVYMHHTPSAASIFPIERRPSPWAMKFRSGHGPAYAEV 484
Qy 485 EPSGHEKEGMEABQC 500
Db 485 EPVG-EKEGFIVSEQ 499

RESULT 3

US-09-912-935-28
; Sequence 28, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912.935
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-28

Query Match 48.1%; Score 1295; DB 9; Length 529;
Best Local Similarity 57.3%; Pred. No. 2.3e-108;
Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;

Qy 72 LAMDTLPDNRTRVVED-NHSYVVSRLYGPSPHSELRVWDVAEANRSOVKIHTILSNTHR 130
Db 95 LLLDDGQDNNTQIEEDTDHNYIISRIYGPSDSASRDLWNIDQMEKDKVKIHGILSNTHR 154
Qy 131 QASRVVLSFDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPYSDNS 190
Db 155 QAARVNLSDFAFVVVHRIQIIPNVRRTIYEHVRLMATAQYIAPLMANFNPYSDNS 214
Qy 191 TVVYFDNGTVFVQWQDHVYLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 250
Db 215 TVRYFDNGTALVQWQDHVYLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQH 274
Qy 251 PVKGLSDAFVNLNPSDPVPSRRSIFRYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 310
Db 275 PVKGLSDAFVNLNPSDPVPSRRSIFRYHRIELDPKSVTSMASAVEFTPLTCLQHRSC 334
Qy 311 DACMSSDLTFNCWCHVLRQCSGSDRYRQWMDGTGCAQAEAGRMCEDFODEDHDSASPD 370
Db 335 GPCVSSQIGFNCWCHVLRQCSGSDRYRQWMDGTGCAQAEAGRMCEDFODEDHDSASPD 394
Qy 371 T--SFSPYDGLTSSS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TIGATTQFRVLTTRRAVTSQFTSLPTEDDTKIALHLKDNASTDDSAEKKGGTLHA 454
Qy 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSTYAEV 484
Db 455 GLVIGLILVILVATAILVTVYMHHTPSAASIFPIERRPSPWAMKFRSGHGPAYAEV 514
Qy 485 EPSGHEKEGMEABQC 500
Db 515 EPVG-EKEGFIVSEQ 529

RESULT 4

US-09-912-935-40
; Sequence 40, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912.935
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53


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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-472

```

Query Match 48.1%; Score 1294; DB 9; Length 529;

Matches	249;	Conservative	73;	Mismatches	106;	Indels	8;	Gaps
QY	72	LAMDLPDNRTRVVD-NHSYYSRLYGSEPHSRSLWVDVAEANRSQVKTIHTLSNTHR	130					
Db	95	LLLDGQDNNTQIEDTDHNYIISRIYGSPDSASRLWNVIDQMEKDKVKLHGILSNTHR	154					
QY	131	QASRVVLGDFDPFYGHPLRQITATGCFIPMGDVIHRLMLTATQYVAPLMAFNFPYSDNS	190					
Db	155	QAARVNLGDFDPFYGHLERLTATGCFITGEVHRLMTATQYIAPLMAFNDFSVSRNS	214					
QY	191	TVYFDNCTVFVQWDHVIYLGQWEDKSGTFFQAALHDCIRTVFAYKEIPMSVPVSSQH	250					
Db	215	TVRYFDNCTALVQWDHVLQDNYNLGSGTFFQATLLMDGRIFGYKEIPVLVYQISSTNH	274					
QY	251	PVKTGLSDAFMLNPSDFVPSRRRSIFEYHRIELDPKSVTSMGSAVEPTPLPTCLOHRSC	310					
Db	275	PVKVLGDAFVYVHRIQQIIPENVRRTIYEHYRVELQMSKITNISAVEMTPLPTCLOFNRC	334					
QY	311	DACMSDILTFCNSCHVLQRCSSGFORYQEWMDYGCQAEAGRMCEDFODEHDGASPD	370					
Db	335	GPCVSSQIGFNCSCWLQRCSSGDFRHHQDWDVSGCPPESEKMKCENTPVTSSRTTT	394					
QY	371	T--SFSPPYDGLTTTS--SSLFIDSLTTEDDTKLNPYAGGDLGLO--NNLSFKTKGTPVHL	424					
Db	395	TVGATTTQFRVLTTRRAVTSQEPPTSLPTEDDTKIALHLKONGASTDDSAEAKGGTLLHA	454					
QY	425	GTIVGIVLAVLLAAIILAGIYINGHPTNNAALFTIERRPHHWPAKFRSHPDHSTYAEV	484					
Db	455	GLIIIGILLVLIVATALLVYVYVHHPTSAASIFFIERRPSRWNPMPFRKSGHPYAEV	514					
QY	485	EPSGHEKEGPFMEAEQC	500					
Db	515	EPVG-EKEGFTVSBQC	529					

RESULT 9

```

US-10-173-706-472
; Sequence 472, Application US/10173706
; Publication No. US2003002293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSFERRED
; TITLE OF INVENTION: ACIDS ENCODING
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-472

```

ORGANISM: Homo Sapien

US-10-173-706-472

Query Match 48.1%; Score 1294; DB 9; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.9e-108;
Matches 249; Conservative 73; Mismatches 106; Indels

Qy	72	LAMDTLPNRTRVVED-NHSTYVSRGLYGPSPHRELWVDVAEANRSQVKIHTILSNTHR	130
Db	95	LLLDGDQDNNTIIEEDTDHNTYIISRIYGPDSASROLDWNIDQMEKDKVKIHTILSNTHR	154
Qy	131	QASRVVLSEDFPEYGHPLROJTIATGGFIEMGDVTHMLTATQYVAPLMAFNPNPGYSDNS	190
Db	155	QAARVNLSEDFPFYGHLEJREJVTATGGFIYGEVHVHMLTATQYIAPLMAFNFPSPVSRNS	214
Qy	191	TVVYFDNGTVPVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAIKEIPMSVPEISSSQH	250
Db	215	TVRVFDNGTALVQWQHDVHLQDNYNLGCSFTFQATLLMDGRIIFYKEIPELVTVQISSTNH	274
Qy	251	PVKGLSDAFMILNPSDPVPSRRRSIFYEHRTELDPKVTYSMSAVEFTPLPTCLOHRSC	310
Db	275	PVKGLSDAFVWVHRIQOIPNVRRTIYEHVRVLEQMSKITNISAVEMTLPPTCLOFNRC	334
Qy	311	DACSSDLTFCNCSMCHVLCRSSGFDTRYROEMWDYGAQAEAGRMCEDFODEDHDSASPD	370
Db	335	GPCVSSQIGFNCSCWKLRCSSGFDHRDWDVDSGCCPEESKEKMCENTEPVTSRITT	394
Qy	371	T--SESPYDGDLLTTS---SSLFIDSJLTEDDTKLNYPYAGDGLQ--NNLSPKTKGTPVHL	424
Db	395	TVGATTTQFRVLTTRRAVTSQEPFSLPTEDDTKIALHLKDNCASTDSDAAEKKGGTLHA	454
Qy	425	GTIVGIVLAVLVAAILAGIYINGHPTSNAAALFFTERPRPHWPAKMFESHDPHSTYAEV	484
Db	455	GLIGILLVLLIVATALLVTVYVHHPTSAASIFFTERRPSRPAMKFRGGSHPAIEV	514
Qy	485	EPSGHEKEGFEAEQC	500
Db	515	EPVG-EKEGFTVSEQ	529

RESULT 10

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US-10-175-738-472
: Sequence 472, Application US/10175738
: Publication No. US20030022294A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: F3430RIC45
: CURRENT APPLICATION NUMBER: US/10/175,738
: CURRENT FILING DATE: 2002-06-19
: Prior application removed - See file Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 472
: LENGTH: 529
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-175-738-472

```

Query Match

Query match	48.18; Score 1294; DB 9;
Best local similarity	57.18; Prod No 2 00-100.

Best Local Similarity 57.1%; Pred. No. 2.9e-108;

	Matches	249; Conservative	73; Mismatches	106; Indels
QY	72	LAMDLPDNRTRVED-NHSYVVSLYCPSEPHSRELWLDVAEANSQVKIHTILSNTHR	13	
D6	95	LLDDGDNNITTEEDTHNYVIRIYSPDSASRLDWNIDQMEKDKYKHGILSNTHR	15	

Db 335 GPCVSSQIGFNCWCKLQRCSSGDRHRQDWDVSGCPESKEKMCENTPEVTSRTTT 394
Qy 371 T--SFSPYDGLTTS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TVGATTQFRVLTTTTRRAVTSQFPTSLPTDDTKLALHLKDNKGASTDDSAAEKKGTLHA 454
Qy 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMPKFRSHPDHSTYAEV 484
Db 455 GLIIGILLVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPMAMPKFRSGHPAYAEV 514
Qy 485 EPSGHEKEGFMAEQ 500
Db 515 EPVG-EKEGFIVSEQ 529

RESULT 13

US-10-176-757-472

; Sequence 472, Application US/10176757

; Publication No. US20030022297A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C86

; CURRENT APPLICATION NUMBER: US/10/176,757

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 472

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-757-472

Query Match 48.1%; Score 1294; DB 9; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.9e-108;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

Qy 72 LAMDTLPNTRRVVED-NHSYVYVSRLYGSPSEPHSRELWVDAEANKRSQVKIHTILSNTHR 130
Db 95 LLLDDGQDNNTQIEEDTHNYIYISRIYGPSDSASRDWVNDQMEKDKVKIHLGILSNTHR 154
Qy 131 QASRVVLSFDFPFYGHPLRQITATGGFIEMGDVTHRLMTATQYVAPLMAFNPNYSN 190
Db 155 QAARVNLSDFFPFYGHPLREITVATGGFIYGEVVRMLTATQYIAPLMAFNPDPSVSRNS 214
Qy 191 TVVYFDNGTVFVVDWVHVYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSOH 250
Db 215 TVRYFDNGTALVVDWVHVHLDQNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTOISSTH 274
Qy 251 PVKTGLSDFAMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRS 310
Db 275 PVKGLSDFAMVWVHRIQIIPNVRRRIYEHVRELQMSKITNISAVEMTPLPTCLOFNRC 334
Qy 311 DACMSSDLTFCNSWCHVLRQCSGDFRYQEWMDYCAOAEGRMCEDFQDEHDSASPD 370
Db 335 GPCVSSQIGFNCWCKLQRCSSGDRHRQDWDVSGCPESKEKMCENTPEVTSRTTT 394
Qy 371 T--SFSPYDGLTTS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TVGATTQFRVLTTTTRRAVTSQFPTSLPTDDTKLALHLKDNKGASTDDSAAEKKGTLHA 454

Qy 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMPKFRSHPDHSTYAEV 484
Db 455 GLIIGILLVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPMAMPKFRSGHPAYAEV 514
Qy 485 EPSGHEKEGFMAEQ 500
Db 515 EPVG-EKEGFIVSEQ 529

RESULT 14

US-10-176-913-472

; Sequence 472, Application US/10176913

; Publication No. US20030022298A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C66

; CURRENT APPLICATION NUMBER: US/10/176,913

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See file Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 472

; LENGTH: 529

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-913-472

Query Match 48.1%; Score 1294; DB 9; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.9e-108;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

Qy 72 LAMDTLPNTRRVVED-NHSYVYVSRLYGSPSEPHSRELWVDAEANKRSQVKIHTILSNTHR 130
Db 95 LLLDDGQDNNTQIEEDTHNYIYISRIYGPSDSASRDWVNDQMEKDKVKIHLGILSNTHR 154
Qy 131 QASRVVLSFDFPFYGHPLRQITATGGFIEMGDVTHRLMTATQYVAPLMAFNPNYSN 190
Db 155 QAARVNLSDFFPFYGHPLREITVATGGFIYGEVVRMLTATQYIAPLMAFNPDPSVSRNS 214
Qy 191 TVVYFDNGTVFVVDWVHVYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSOH 250
Db 215 TVRYFDNGTALVVDWVHVHLDQNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTOISSTH 274
Qy 251 PVKTGLSDFAMILNPSDPVPSRRRSIFEYHRIELDPKVTSMASAVEFTPLPTCLOHRS 310
Db 275 PVKGLSDFAMVWVHRIQIIPNVRRRIYEHVRELQMSKITNISAVEMTPLPTCLOFNRC 334
Qy 311 DACMSSDLTFCNSWCHVLRQCSGDFRYQEWMDYCAOAEGRMCEDFQDEHDSASPD 370
Db 335 GPCVSSQIGFNCWCKLQRCSSGDRHRQDWDVSGCPESKEKMCENTPEVTSRTTT 394
Qy 371 T--SFSPYDGLTTS---SSLFIDSLTDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TVGATTQFRVLTTTTRRAVTSQFPTSLPTDDTKLALHLKDNKGASTDDSAAEKKGTLHA 454
Qy 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMPKFRSHPDHSTYAEV 484
Db 455 GLIIGILLVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPMAMPKFRSGHPAYAEV 514
Qy 485 EPSGHEKEGFMAEQ 500
Db 515 EPVG-EKEGFIVSEQ 529

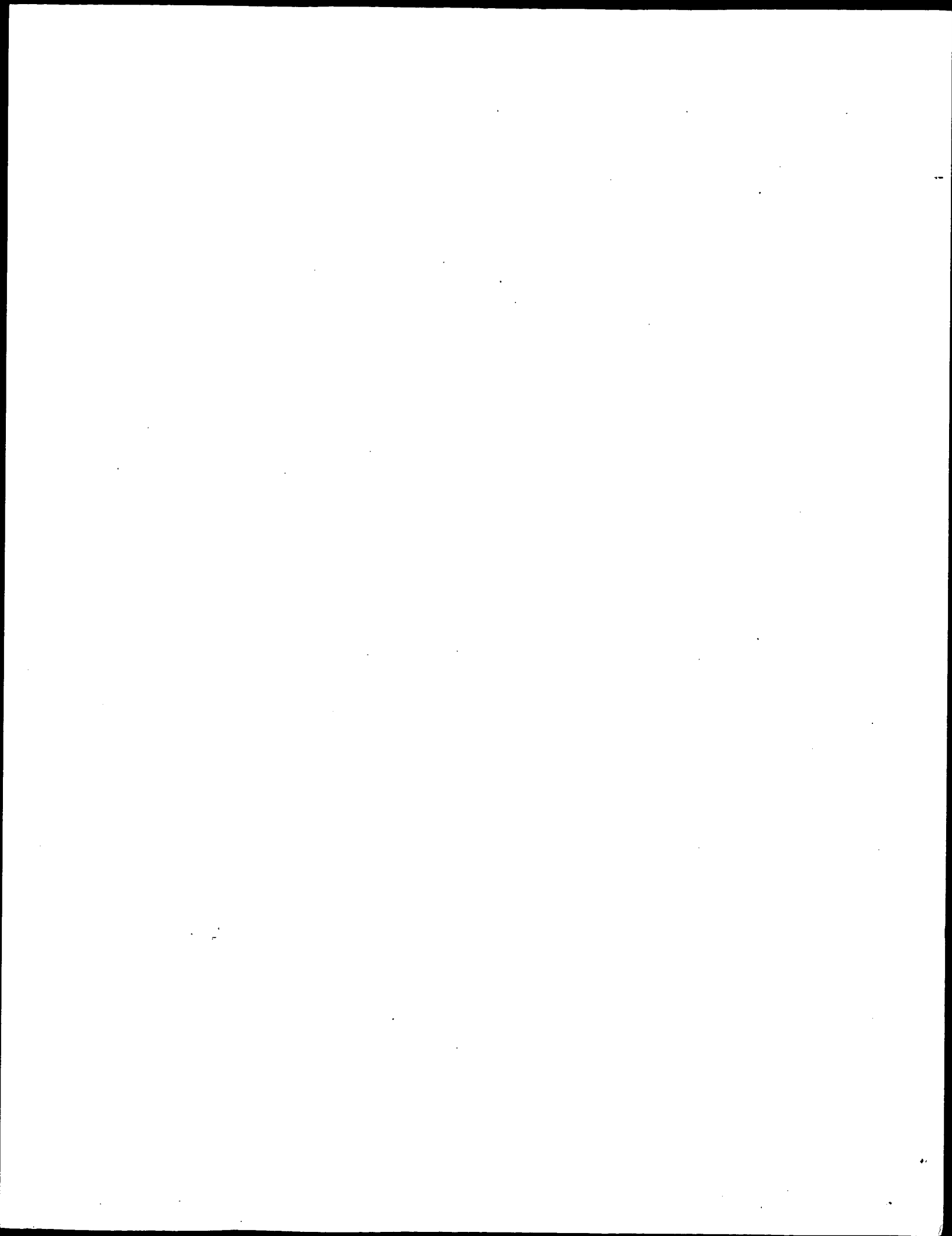
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RESULT 15
US-10-180-552-472
; Sequence 472, Application US/10180552
; Publication No. US20030022300A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC153
; CURRENT APPLICATION NUMBER: US/10/180.552
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-180-552-472

Query Match      48.1%; Score 1294; DB 9; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.9e-108;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVED-NHSYVYSLYGPSEPHSLWVDVAEANSQVKIHTILSNTHR 130
DB 95 LLLDDGQDNTQIEDTHNYIYISRIYGPSDSASRDVWNIIDOMEKDKVKINGILSNTHR 154
QY 131 QASRVVLSDFPFYGHPLRQITATGGFIFMGDVTHRLMTATQYVAPLMAFNENPGYSNDS 190
DB 155 QAARVNLSPDFPFYGHFLREITVATGGFTYGEVHRLMTATQYIAPLMAFNDFPSVRNS 214
QY 191 TVYFNGVYVQVQDHVYVLOGWEKGSFTFOALHHDGRIVFAYKEIPMSVPEISSQOH 250
DB 215 TVYFNGVYVQVQDHVYVLOGWEKGSFTFOALHHDGRIVFAYKEIPMSVPEISSQOH 274
QY 251 PVKTLGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPLTCLQHRSC 310
DB 275 PVKTLGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTPLTCLQHRSC 334
QY 311 DACMSSDLFNCSWCHVLOKSCGGEDRYQENMDYCAQEAERWCEDEDFODEDHDSPD 370
DB 335 GPCVSSQIGFNCSCWCKLQKSCGGEDRYQENMDYCAQEAERWCEDEDFODEDHDSPD 394
QY 371 T--SFSPIYDGLTTS---SSLFIDSLTDEDDTKLNPYAGDGLQ--NNLSPKTKGTPVHL 424
DB 395 TVGATTQFVLTTRAVTSQPTSLPTEDDTKIALHLKDNKASTDSDAAEKKGGTLHA 454
QY 425 GTTIVGLVAVLLAGIYINGHTPSNAALFFIERRPHHWPAMKFRSHDPDHYAEV 484
DB 455 GLIIGILLVIVATILVTVVYHHPTSAASIFFIERRPSRWPAMKFRRGSGHPAYAEV 514
QY 485 EPSGHEKEGFMEAEQC 500
DB 515 EPVG-EKGGFIVSEQC 529
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Search completed: April 22, 2003, 16:15:41
Job time : 45 secs



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:18:56 ; Search time 20 Seconds
(without alignments)
2003.245 Million cell updates/sec

Title: US-09-918-715-230
Perfect score: 500
Sequence: 1 MKGELWLLVLVLRARALS.....YAEVEPSGHEKEGFMEARQC 500

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 301932 seqs, 80129803 residues

Word size : 0
Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications_AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	271	54.2	431	9	US-09-912-935-36
2	53	10.6	53	10	US-09-864-761-43750
3	10	2.0	118	10	US-09-867-550-198
4	10	2.0	392	9	US-09-912-935-23
5	10	2.0	392	9	US-09-912-935-25
6	10	2.0	425	9	US-09-912-935-35
7	10	2.0	449	9	US-09-912-935-34
8	10	2.0	499	9	US-09-912-935-31
9	10	2.0	529	9	US-10-066-500-128
10	10	2.0	529	9	US-10-174-590-472
11	10	2.0	529	9	US-10-176-758-472
12	10	2.0	529	9	US-10-175-737-472
13	10	2.0	529	9	US-09-912-935-28
14	10	2.0	529	9	US-09-912-935-40
15	10	2.0	529	9	US-10-173-706-472
16	10	2.0	529	9	US-10-175-738-472
17	10	2.0	529	9	US-10-175-752-472
18	10	2.0	529	9	US-10-176-482-472
19	10	2.0	529	9	US-10-176-757-472

20	10	2.0	529	9	US-10-176-913-472	Sequence 472, App
21	10	2.0	529	9	US-10-180-552-472	Sequence 472, App
22	10	2.0	529	9	US-10-180-557-472	Sequence 472, App
23	10	2.0	529	9	US-10-173-700-472	Sequence 472, App
24	10	2.0	529	9	US-10-174-572-472	Sequence 472, App
25	10	2.0	529	9	US-10-174-579-472	Sequence 472, App
26	10	2.0	529	9	US-10-174-582-472	Sequence 472, App
27	10	2.0	529	9	US-10-174-588-472	Sequence 472, App
28	10	2.0	529	9	US-10-175-739-472	Sequence 472, App
29	10	2.0	529	9	US-10-175-743-472	Sequence 472, App
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32	10	2.0	529	9	US-10-176-492-472	Sequence 472, App
33	10	2.0	529	9	US-10-176-747-472	Sequence 472, App
34	10	2.0	529	9	US-10-176-750-472	Sequence 472, App
35	10	2.0	529	9	US-10-176-985-472	Sequence 472, App
36	10	2.0	529	9	US-10-176-987-472	Sequence 472, App
37	10	2.0	529	9	US-10-176-991-472	Sequence 472, App
38	10	2.0	529	9	US-10-176-992-472	Sequence 472, App
39	10	2.0	529	9	US-10-176-993-472	Sequence 472, App
40	10	2.0	529	9	US-10-184-658-472	Sequence 472, App
41	10	2.0	529	9	US-10-002-796-128	Sequence 128, App
42	10	2.0	529	9	US-10-066-273-128	Sequence 128, App
43	10	2.0	529	9	US-10-066-494-128	Sequence 128, App
44	10	2.0	529	9	US-10-173-695-472	Sequence 472, App
45	10	2.0	529	9	US-10-173-705-472	Sequence 472, App
46	10	2.0	529	9	US-10-174-576-472	Sequence 472, App
47	10	2.0	529	9	US-10-174-585-472	Sequence 472, App
48	10	2.0	529	9	US-10-174-586-472	Sequence 472, App
49	10	2.0	529	9	US-10-175-747-472	Sequence 472, App
50	10	2.0	529	9	US-10-176-481-472	Sequence 472, App
51	10	2.0	529	9	US-10-176-485-472	Sequence 472, App
52	10	2.0	529	9	US-10-176-487-472	Sequence 472, App
53	10	2.0	529	9	US-10-176-493-472	Sequence 472, App
54	10	2.0	529	9	US-10-176-756-472	Sequence 472, App
55	10	2.0	529	9	US-10-176-911-472	Sequence 472, App
56	10	2.0	529	9	US-10-176-925-472	Sequence 472, App
57	10	2.0	529	9	US-10-176-978-472	Sequence 472, App
58	10	2.0	529	9	US-10-179-510-472	Sequence 472, App
59	10	2.0	529	9	US-10-180-543-472	Sequence 472, App
60	10	2.0	529	9	US-10-180-544-472	Sequence 472, App
61	10	2.0	529	9	US-10-180-546-472	Sequence 472, App
62	10	2.0	529	9	US-10-180-547-472	Sequence 472, App
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64	10	2.0	529	9	US-10-180-554-472	Sequence 472, App
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69	10	2.0	529	9	US-10-183-012-472	Sequence 472, App
70	10	2.0	529	9	US-10-184-614-472	Sequence 472, App
71	10	2.0	529	9	US-10-184-623-472	Sequence 472, App
72	10	2.0	529	9	US-10-184-635-472	Sequence 472, App
73	10	2.0	529	9	US-10-184-646-472	Sequence 472, App
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81	10	2.0	529	9	US-10-199-464-472	Sequence 472, App
82	10	2.0	529	9	US-10-176-751-472	Sequence 472, App
83	10	2.0	529	9	US-10-176-760-472	Sequence 472, App
84	10	2.0	529	9	US-10-176-990-472	Sequence 472, App
85	10	2.0	529	9	US-10-180-541-472	Sequence 472, App
86	10	2.0	529	9	US-10-180-542-472	Sequence 472, App
87	10	2.0	529	9	US-10-180-548-472	Sequence 472, App
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89	10	2.0	529	9	US-10-180-998-472	Sequence 472, App
90	10	2.0	529	9	US-10-180-999-472	Sequence 472, App
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92	10	2.0	529	9	US-10-180-999-472	Sequence 472, App

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94	10	2.0	529	9	US-10-184-612-472	Sequence 472, App	167	10	2.0	529	9	US-10-176-753-472	Sequence 472, App
95	10	2.0	529	9	US-10-184-616-472	Sequence 472, App	168	10	2.0	529	9	US-10-176-917-472	Sequence 472, App
96	10	2.0	529	9	US-10-184-617-472	Sequence 472, App	169	10	2.0	529	9	US-10-176-982-472	Sequence 472, App
97	10	2.0	529	9	US-10-184-622-472	Sequence 472, App	170	10	2.0	529	9	US-10-179-506-472	Sequence 472, App
98	10	2.0	529	9	US-10-184-628-472	Sequence 472, App	171	10	2.0	529	9	US-10-179-513-472	Sequence 472, App
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102	10	2.0	529	9	US-10-184-632-472	Sequence 472, App	175	10	2.0	529	9	US-10-180-560-472	Sequence 472, App
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105	10	2.0	529	9	US-10-184-650-472	Sequence 472, App	178	10	2.0	529	9	US-10-184-620-472	Sequence 472, App
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109	10	2.0	529	9	US-10-187-598-472	Sequence 472, App	182	10	2.0	529	9	US-10-195-894-472	Sequence 472, App
110	10	2.0	529	9	US-10-187-601-472	Sequence 472, App	183	10	2.0	529	9	US-10-205-908-472	Sequence 472, App
111	10	2.0	529	9	US-10-187-602-472	Sequence 472, App	184	10	2.0	529	9	US-10-184-619-472	Sequence 472, App
112	10	2.0	529	9	US-10-187-603-472	Sequence 472, App	185	10	2.0	529	9	US-10-186-855-472	Sequence 472, App
113	10	2.0	529	9	US-10-187-741-472	Sequence 472, App	186	10	2.0	529	9	US-10-187-599-472	Sequence 472, App
114	10	2.0	529	9	US-10-187-743-472	Sequence 472, App	187	10	2.0	529	9	US-10-187-750-472	Sequence 472, App
115	10	2.0	529	9	US-10-187-746-472	Sequence 472, App	188	10	2.0	529	9	US-10-188-780-472	Sequence 472, App
116	10	2.0	529	9	US-10-187-747-472	Sequence 472, App	189	10	2.0	529	9	US-10-192-015-472	Sequence 472, App
117	10	2.0	529	9	US-10-187-751-472	Sequence 472, App	190	10	2.0	529	9	US-10-194-394-472	Sequence 472, App
118	10	2.0	529	9	US-10-187-753-472	Sequence 472, App	191	10	2.0	529	9	US-10-194-425-472	Sequence 472, App
119	10	2.0	529	9	US-10-187-754-472	Sequence 472, App	192	10	2.0	529	9	US-10-194-485-472	Sequence 472, App
120	10	2.0	529	9	US-10-187-757-472	Sequence 472, App	193	10	2.0	529	9	US-10-195-885-472	Sequence 472, App
121	10	2.0	529	9	US-10-187-884-472	Sequence 472, App							

531	6	1.2	89	10	US-09-915-582-76	Sequence 76, Appl	604	1.2	226	9	US-09-992-598-151	Sequence 151, App
532	6	1.2	90	9	US-10-083-357-1282	Sequence 1282, Ap	605	1.2	226	9	US-09-989-293A-151	Sequence 151, App
533	6	1.2	91	9	US-09-738-626-6912	Sequence 6912, Ap	606	1.2	226	9	US-09-989-735-151	Sequence 151, App
534	6	1.2	92	10	US-09-939-980-340	Sequence 340, App	607	1.2	226	9	US-09-990-444-151	Sequence 151, App
535	6	1.2	93	10	US-09-764-864-1203	Sequence 1203, Ap	608	1.2	226	9	US-09-989-730-151	Sequence 151, App
536	6	1.2	98	12	US-10-001-879-146	Sequence 146, App	609	1.2	226	9	US-09-990-436-151	Sequence 151, App
537	6	1.2	99	10	US-09-864-761-42807	Sequence 42807, A	610	1.2	226	9	US-09-991-181-151	Sequence 151, App
538	6	1.2	100	9	US-10-045-180A-11	Sequence 11, Appl	611	1.2	226	9	US-09-993-687-151	Sequence 151, App
539	6	1.2	104	10	US-09-864-761-45427	Sequence 45427, A	612	1.2	226	9	US-09-989-734-151	Sequence 151, App
540	6	1.2	105	9	US-10-091-504-1175	Sequence 1175, Ap	613	1.2	226	9	US-09-997-653-151	Sequence 151, App
541	6	1.2	103	10	US-09-764-869-1175	Sequence 1175, Ap	614	1.2	226	9	US-10-174-590-122	Sequence 122, App
542	6	1.2	107	10	US-09-867-550-282	Sequence 282, App	615	1.2	226	9	US-10-176-758-122	Sequence 122, App
543	6	1.2	109	9	US-09-796-692-2460	Sequence 2460, Ap	616	1.2	226	9	US-10-175-737-122	Sequence 122, App
544	6	1.2	109	10	US-09-864-761-33601	Sequence 33601, A	617	1.2	226	9	US-09-993-606-151	Sequence 151, App
545	6	1.2	112	9	US-10-101-464A-535	Sequence 535, App	618	1.2	226	9	US-10-175-738-122	Sequence 122, App
546	6	1.2	117	9	US-09-949-842-17	Sequence 17, Appl	619	1.2	226	9	US-10-176-482-122	Sequence 122, App
547	6	1.2	121	9	US-09-738-626-4106	Sequence 4106, Ap	620	1.2	226	9	US-10-176-757-122	Sequence 122, App
548	6	1.2	121	9	US-09-820-843A-118	Sequence 118, App	621	1.2	226	9	US-10-176-737-122	Sequence 122, App
549	6	1.2	121	10	US-09-925-297-791	Sequence 791, App	622	1.2	226	9	US-10-175-738-122	Sequence 122, App
550	6	1.2	122	9	US-10-125-540-321	Sequence 321, App	623	1.2	226	9	US-10-175-738-122	Sequence 122, App
551	6	1.2	122	10	US-09-764-870-321	Sequence 321, App	624	1.2	226	9	US-10-175-738-122	Sequence 122, App
552	6	1.2	122	10	US-09-764-853-636	Sequence 636, App	625	1.2	226	9	US-10-176-482-122	Sequence 122, App
553	6	1.2	122	10	US-09-925-300-1438	Sequence 1438, Ap	626	1.2	226	9	US-10-176-757-122	Sequence 122, App
554	6	1.2	125	9	US-09-918-508-7	Sequence 7, Appl	627	1.2	226	9	US-10-176-737-122	Sequence 122, App
555	6	1.2	132	9	US-09-975-036-9	Sequence 9, Appl	628	1.2	226	9	US-10-176-737-122	Sequence 122, App
556	6	1.2	133	9	US-09-738-626-6531	Sequence 6531, Ap	629	1.2	226	9	US-09-990-562-151	Sequence 151, App
557	6	1.2	135	10	US-09-864-761-36267	Sequence 36267, A	630	1.2	226	9	US-09-997-428-151	Sequence 151, App
558	6	1.2	136	10	US-09-833-017-23	Sequence 23, Appl	631	1.2	226	9	US-09-997-666-151	Sequence 151, App
559	6	1.2	137	10	US-09-925-301-1519	Sequence 1519, Ap	632	1.2	226	9	US-10-173-700-122	Sequence 122, App
560	6	1.2	143	10	US-09-867-550-1866	Sequence 1866, Ap	633	1.2	226	9	US-10-174-572-122	Sequence 122, App
561	6	1.2	147	9	US-10-091-504-1109	Sequence 1109, Ap	634	1.2	226	9	US-10-174-572-122	Sequence 122, App
562	6	1.2	147	10	US-09-764-869-1109	Sequence 1109, Ap	635	1.2	226	9	US-10-174-582-122	Sequence 122, App
563	6	1.2	148	9	US-09-975-4568-5	Sequence 5, Appl	636	1.2	226	9	US-10-174-588-122	Sequence 122, App
564	6	1.2	150	9	US-10-078-770-130	Sequence 130, App	637	1.2	226	9	US-10-175-739-122	Sequence 122, App
565	6	1.2	153	10	US-09-822-635-5	Sequence 5, Appl	638	1.2	226	9	US-10-175-740-122	Sequence 122, App
566	6	1.2	153	10	US-09-800-971-6	Sequence 6, Appl	639	1.2	226	9	US-10-175-743-122	Sequence 122, App
567	6	1.2	153	10	US-09-927-112-7	Sequence 7, Appl	640	1.2	226	9	US-10-176-492-122	Sequence 122, App
568	6	1.2	153	10	US-09-908-664-19	Sequence 19, Appl	641	1.2	226	9	US-10-176-492-122	Sequence 122, App
569	6	1.2	153	10	US-09-908-664-19	Sequence 19, Appl	642	1.2	226	9	US-10-176-492-122	Sequence 122, App
570	6	1.2	155	9	US-09-738-626-6458	Sequence 6458, Ap	643	1.2	226	9	US-10-176-750-122	Sequence 122, App
571	6	1.2	156	10	US-09-925-297-511	Sequence 511, App	644	1.2	226	9	US-10-176-987-122	Sequence 122, App
572	6	1.2	157	9	US-10-108-605-153	Sequence 153, App	645	1.2	226	9	US-10-176-991-122	Sequence 122, App
573	6	1.2	157	10	US-09-894-018-117	Sequence 117, App	646	1.2	226	9	US-10-176-992-122	Sequence 122, App
574	6	1.2	162	10	US-09-864-761-42286	Sequence 42286, A	647	1.2	226	9	US-10-176-992-122	Sequence 122, App
575	6	1.2	162	10	US-09-747-155-306	Sequence 306, App	648	1.2	226	9	US-10-184-658-122	Sequence 122, App
576	6	1.2	163	9	US-10-050-704-120	Sequence 120, App	649	1.2	226	9	US-09-990-711-151	Sequence 151, App
577	6	1.2	165	10	US-09-938-970-6	Sequence 6, Appl	650	1.2	226	9	US-10-173-697-122	Sequence 122, App
578	6	1.2	170	9	US-09-738-626-6851	Sequence 6851, Ap	651	1.2	226	9	US-10-173-705-122	Sequence 122, App
579	6	1.2	181	10	US-09-942-446-6	Sequence 6, Appl	652	1.2	226	9	US-10-174-576-122	Sequence 122, App
580	6	1.2	191	10	US-09-811-284-257	Sequence 257, App	653	1.2	226	9	US-10-174-585-122	Sequence 122, App
581	6	1.2	193	10	US-09-864-761-34864	Sequence 34864, A	654	1.2	226	9	US-10-174-585-122	Sequence 122, App
582	6	1.2	196	10	US-09-811-284-183	Sequence 183, Appl	655	1.2	226	9	US-10-174-586-122	Sequence 122, App
583	6	1.2	197	10	US-09-905-114-2	Sequence 2, Appl	656	1.2	226	9	US-10-175-747-122	Sequence 122, App
584	6	1.2	198	9	US-09-791-279-200	Sequence 200, App	657	1.2	226	9	US-10-176-481-122	Sequence 122, App
585	6	1.2	198	10	US-09-864-761-37569	Sequence 37569, A	658	1.2	226	9	US-10-176-485-122	Sequence 122, App
586	6	1.2	198	10	US-09-867-550-766	Sequence 766, App	659	1.2	226	9	US-10-176-487-122	Sequence 122, App
587	6	1.2	199	10	US-09-911-346-17	Sequence 17, Appl	660	1.2	226	9	US-10-176-493-122	Sequence 122, App
588	6	1.2	202	9	US-10-050-704-251	Sequence 251, App	661	1.2	226	9	US-10-176-911-122	Sequence 122, App
589	6	1.2	206	9	US-09-738-626-6923	Sequence 6923, Ap	662	1.2	226	9	US-10-176-911-122	Sequence 122, App
590	6	1.2	209	10	US-09-761-534A-12	Sequence 12, Appl	663	1.2	226	9	US-10-176-925-122	Sequence 122, App
591	6	1.2	210	10	US-09-761-534A-8	Sequence 8, Appl	664	1.2	226	9	US-10-176-978-122	Sequence 122, App
592	6	1.2	211	9	US-09-731-449-14	Sequence 14, Appl	665	1.2	226	9	US-10-179-510-122	Sequence 122, App
593	6	1.2	211	9	US-09-731-449-41	Sequence 41, Appl	666	1.2	226	9	US-10-180-543-122	Sequence 122, App
594	6	1.2	211	9	US-09-731-449-49	Sequence 49, Appl	667	1.2	226	9	US-10-180-543-122	Sequence 122, App
595	6	1.2	213	10	US-09-771-209-14	Sequence 14, Appl	668	1.2	226	9	US-10-180-546-122	Sequence 122, App
596	6	1.2	214	9	US-09-738-626-4679	Sequence 4679, Ap	669	1.2	226	9	US-10-180-547-122	Sequence 122, App
597	6	1.2	215	10	US-09-925-297-660	Sequence 660, App	670	1.2	226	9	US-10-180-549-122	Sequence 122, App
598	6	1.2	221	9	US-09-738-626-6107	Sequence 6107, Ap	671	1.2	226	9	US-10-180-555-122	Sequence 122, App
599	6	1.2	222	9	US-10-092-925-2	Sequence 2, Appl	672	1.2	226	9	US-10-180-555-122	Sequence 122, App
600	6	1.2	222	10	US-09-897-772-2	Sequence 8, Appl	673	1.2	226	9	US-10-180-559-122	Sequence 122, App
601	6	1.2	223	9	US-09-811-088-8	Sequence 8, Appl	674	1.2	226	9	US-10-181-000-122	Sequence 122, App
602	6	1.2	223	9	US-10-062-523-19	Sequence 19, Appl	675	1.2	226	9	US-10-183-010-122	Sequence 122, App
603	6	1.2	224	10	US-09-764-864-1465	Sequence 1465, Ap	676	1.2	226	9		

969 6 1.2 226 9 US-10-206-912-122 Sequence 122, App
970 6 1.2 226 9 US-10-206-913-122 Sequence 122, App
971 6 1.2 226 9 US-10-206-914-122 Sequence 122, App
972 6 1.2 226 9 US-10-206-920-122 Sequence 122, App
973 6 1.2 226 9 US-10-206-921-122 Sequence 122, App
974 6 1.2 226 9 US-10-206-923-122 Sequence 122, App
975 6 1.2 226 9 US-10-206-925-122 Sequence 122, App
976 6 1.2 226 9 US-10-206-926-122 Sequence 122, App
977 6 1.2 226 9 US-10-206-927-122 Sequence 122, App
978 6 1.2 226 9 US-10-207-916-122 Sequence 122, App
979 6 1.2 226 9 US-10-207-917-122 Sequence 122, App
980 6 1.2 226 9 US-10-207-918-122 Sequence 122, App
981 6 1.2 226 9 US-10-207-919-122 Sequence 122, App
982 6 1.2 226 9 US-10-207-920-122 Sequence 122, App
983 6 1.2 226 9 US-10-207-925-122 Sequence 122, App
984 6 1.2 226 9 US-10-208-021-122 Sequence 122, App
985 6 1.2 226 9 US-10-208-022-122 Sequence 122, App
986 6 1.2 226 9 US-10-208-023-122 Sequence 122, App
987 6 1.2 226 9 US-10-208-026-122 Sequence 122, App
988 6 1.2 226 9 US-10-208-029-122 Sequence 122, App
989 6 1.2 226 9 US-10-208-030-122 Sequence 122, App
990 6 1.2 226 9 US-10-232-232-122 Sequence 122, App
991 6 1.2 226 9 US-09-990-427-151 Sequence 151, App
992 6 1.2 226 9 US-09-990-439-151 Sequence 151, App
993 6 1.2 226 9 US-10-173-693-122 Sequence 122, App
994 6 1.2 226 9 US-10-174-578-122 Sequence 122, App
995 6 1.2 226 9 US-10-175-741-122 Sequence 122, App
996 6 1.2 226 9 US-10-175-750-122 Sequence 122, App
997 6 1.2 226 9 US-10-176-986-122 Sequence 122, App
998 6 1.2 226 9 US-10-184-641-122 Sequence 122, App
999 6 1.2 226 9 US-10-187-888-122 Sequence 122, App
1000 6 1.2 226 10 US-09-990-456-151 Sequence 151, App

ALIGNMENTS

RESULT 1
US-09-912-935-36
; Sequence 36, Application US/09912935
; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-36

Query Match 54.2%; Score 271; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.2e-247;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 LAMDTLPDNRTRVEDNHNHYSVRLYGPSPHSHRELVWDVAEANRSQVKIHILTSNTHRQ 131
Db 1 LAMDTLPDNRTRVEDNHNHYSVRLYGPSPHSHRELVWDVAEANRSQVKIHILTSNTHRQ 60
QY 132 ASRVLSFDPFPYGHPLRQITTIATGGFIEMGDVHRLMTATQVAPLMAFNPNFYSDNST 191
Db 61 ASRVLSFDPFPYGHPLRQITTIATGGFIEMGDVHRLMTATQVAPLMAFNPNFYSDNST 120
QY 192 VVYFNGTVEVQWDHYVLOGWEDKGSFTFOALHHDGRIVFAYKIPMSVPEISSQHP 251
Db 121 VVYFNGTVEVQWDHYVLOGWEDKGSFTFOALHHDGRIVFAYKIPMSVPEISSQHP 180

QY 252 VKTCLSDAFMILLNPSPDVPSPRRRSIFEXYHRIELDPKVTSMSSAVFTPLPTCLQHRSCD 311
Db 181 VKTCLSDAFMILLNPSPDVPSPRRRSIFEXYHRIELDPKVTSMSSAVFTPLPTCLQHRSCD 240
QY 312 ACMSSDLTFNCSCWCHVLQRCSSGFDYRQEW 342
Db 241 ACMSSDLTFNCSCWCHVLQRCSSGFDYRQEW 271

RESULT 2
US-09-864-761-43750
; Sequence 43750, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weusheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43750
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004408.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.97
OTHER INFORMATION: EST_HUMAN HIT: AW028265.1, EVALUE 2.00e-26
OTHER INFORMATION: SWISSPROT HIT: Q09530, EVALUE 3.60e+00
US-09-864-761-43750

Query Match 10.6%; Score 53; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.3e-42; Indels 0;
Matches 53; Conservative 0; Mismatches 0; Gaps 0;

QY 27 HDEPGSGWAAGTGVGNRRARESPCHVSEPDRTQLSQDLGGTTLAMDTPD 79
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Db 1 HDEPGSGWAAGTGVGNRRARESPCHVSEPDRTQLSQDLGGTTLAMDTPD 53

RESULT 3

US-09-867-550-198
Sequence 198, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-09-867-550-198

Query Match 2.0%; Score 10; DB 10; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

QY 137 LSFDFPFYGH 146
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Db 47 LSFDFPFYGH 56

RESULT 4

US-09-912-935-23
Sequence 23, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-23

Query Match 2.0%; Score 10; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

QY 137 LSFDFPFYGH 146
|||||
Db 24 LSFDFPFYGH 33

RESULT 5

US-09-912-935-25
Sequence 25, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-25

Query Match 2.0%; Score 10; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

QY 137 LSFDFPFYGH 146
|||||
Db 24 LSFDFPFYGH 33

RESULT 6

US-09-912-935-35
Sequence 35, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 35
LENGTH: 425
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-35

Query Match 2.0%; Score 10; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.33; Indels 0;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;

QY 137 LSFDFPFYGH 146
|||||
Db 59 LSFDFPFYGH 68

RESULT 7

US-09-912-935-34
Sequence 34, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE

FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-34

Query Match 2.0%; Score 10; DB 9; Length 449;

Best Local Similarity 100.0%; Pred. No. 0.35;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146

Db 161 LSFDFPFYGH 170

RESULT 8

US-09-912-935-31

Sequence 31, Application US/09912935

Publication No. US2003002825A1

GENERAL INFORMATION:

APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: PCT/US00/35260

PRIOR FILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn version 3.0

SEQ ID NO 31

LENGTH: 499

TYPE: PRT

ORGANISM: Homo sapiens

US-09-912-935-31

Query Match 2.0%; Score 10; DB 9; Length 499;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146

Db 131 LSFDFPFYGH 140

RESULT 9

US-10-066-500-128

Sequence 128, Application US/10066500

Patent No. US20020177165A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi

APPLICANT: Kevin P. Baker

APPLICANT: David A. Botstein

APPLICANT: Luc Desnoyers

APPLICANT: Dan L. Eaton

APPLICANT: Napoleone Ferrara

APPLICANT: Sherman Fong

APPLICANT: Wei-Qiang Gao

APPLICANT: Hanspeter Gerber

APPLICANT: Mary E. Gerritsen

APPLICANT: Audrey Goddard

APPLICANT: Paul J. Godowski

APPLICANT: Austin L. Gurney

APPLICANT: Ivar J. Kljavin

APPLICANT: Jennie P. Mather

APPLICANT: Mary A. Napier

APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P31301C7
CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
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PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 09/866028
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 ; PRIOR APPLICATION NUMBER: PCT/US98/14552
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 ; PRIOR APPLICATION NUMBER: PCT/US98/18824
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: PCT/US98/19093
 ; PRIOR FILING DATE: 1998-09-14
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: PCT/US98/19437
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: PCT/US98/24855
 ; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108
 ; PRIOR FILING DATE: 1998-12-01
 ; PRIOR APPLICATION NUMBER: PCT/US98/25190
 ; PRIOR FILING DATE: 1998-11-25
 ; PRIOR APPLICATION NUMBER: PCT/US99/05028
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 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: 1999-06-02
 ; PRIOR APPLICATION NUMBER: PCT/US99/20111
 ; PRIOR FILING DATE: 1999-09-01
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594
 ; PRIOR FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 2.0%; Score 10; DB 9; Length 529;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
 DB 161 LSFDFPFYGH 170

RESULT 10

US-10-174-590-472
 ; Sequence 472, Application US/10174590
 ; Publication No. US20030008352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430RIC42
 ; CURRENT APPLICATION NUMBER: US/10/174,590
 ; CURRENT FILING DATE: 2002-06-18
 ; Prior application removed - See file Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 472
 ; LENGTH: 529
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-174-590-472

Query Match 2.0%; Score 10; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
Db 161 LSFDFPFYGH 170

RESULT 11

US-10-176-758-472
; Sequence 472, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-176-758-472

Query Match 2.0%; Score 10; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
Db 161 LSFDFPFYGH 170

RESULT 12

US-10-175-737-472
; Sequence 472, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
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; LENGTH: 529

; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-472

Query Match 2.0%; Score 10; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
Db 161 LSFDFPFYGH 170

RESULT 13

US-09-912-935-28
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; Publication No. US20030022825A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
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US-09-912-935-28

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Db 161 LSFDFPFYGH 170

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; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
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US-09-912-935-40

Query Match 2.0%; Score 10; DB 9; Length 529;
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QY 137 LSFDFPFYGH 146
Db 161 LSFDFPFYGH 170

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; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
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; ORGANISM: Homo Sapien
US-10-173-706-472

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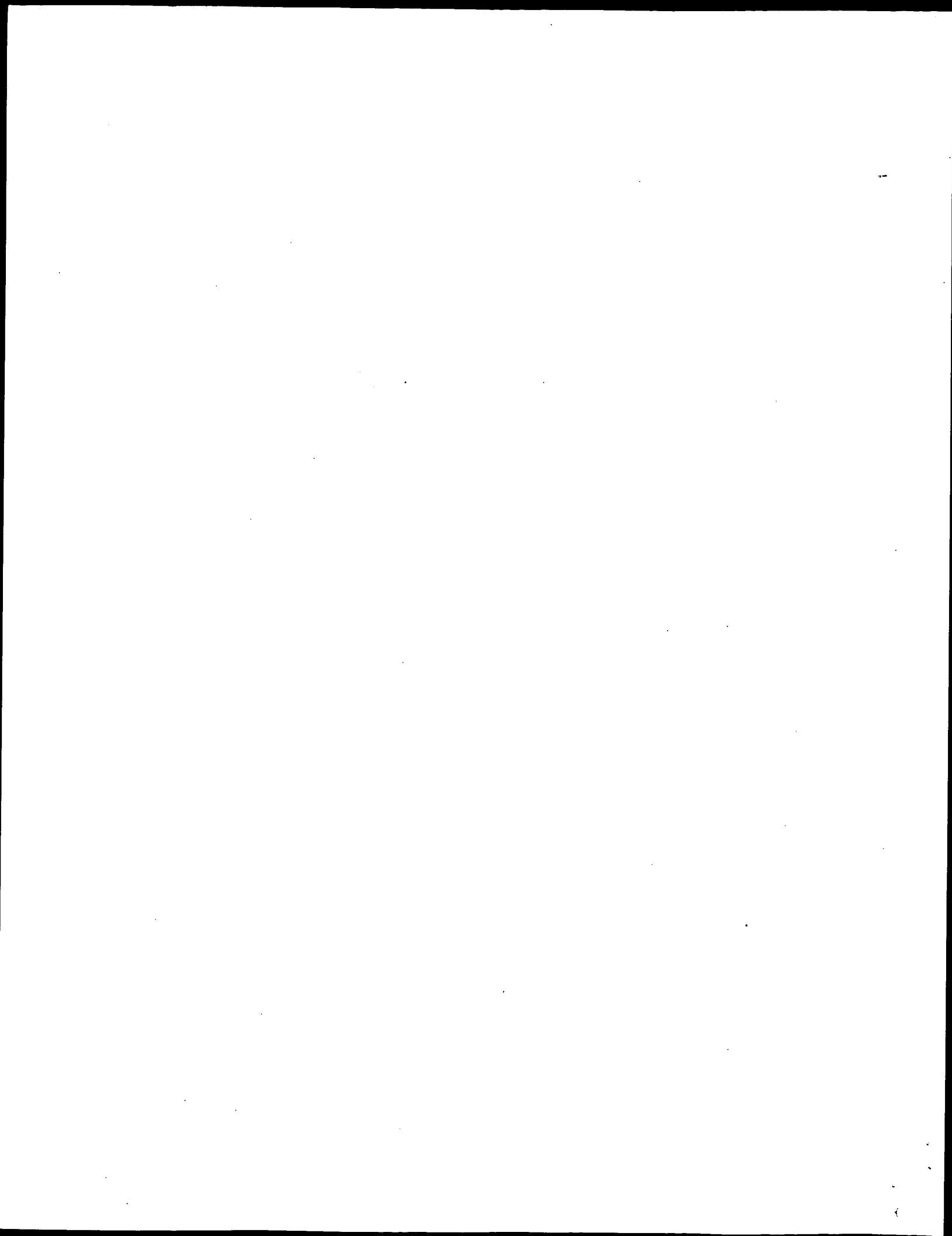
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2691	100.0	500	1 PCT-US02-08253-230
3	2691	100.0	500	1 PCT-US02-29964-314
4	2691	100.0	500	23 US-09-918-715-230
5	2691	100.0	500	27 US-60-327-731-5
6	2691	100.0	500	27 US-60-327-731-15

7	2691	100.0	527	1	PCT-US02-29964-804	Sequence 804, App
8	2691	100.0	527	1	PCT-US02-29964-805	Sequence 805, App
9	2691	100.0	527	27	US-60-327-731-3	Sequence 3, Appli
10	2691	100.0	1002	1	PCT-US01-24031-179	Sequence 179, App
11	2691	100.0	1002	1	PCT-US02-08253-179	Sequence 179, App
12	2691	100.0	1002	23	US-09-918-715-179	Sequence 179, App
13	2607	96.9	488	1	PCT-US02-29964-315	Sequence 315, App
14	2607	96.9	488	27	US-60-327-731-10	Sequence 10, Appl
15	2604	96.8	482	27	US-60-327-731-8	Sequence 8, Appli
16	2566	95.4	502	1	PCT-US02-16639-5	Sequence 5, Appli
17	2566	95.4	502	25	US-10-156-487A-5	Sequence 12, Appl
18	2520	93.6	470	27	US-60-327-731-12	Sequence 12, App
19	2209	82.1	500	1	PCT-US01-24031-192	Sequence 192, App
20	2209	82.1	500	1	PCT-US01-24031-297	Sequence 192, App
21	2209	82.1	500	1	PCT-US02-08253-192	Sequence 192, App
22	2209	82.1	500	1	PCT-US02-08253-297	Sequence 297, App
23	2209	82.1	500	1	PCT-US02-16639-6	Sequence 6, Appli
24	2209	82.1	500	23	US-09-918-715-192	Sequence 192, App
25	2209	82.1	500	23	US-09-918-715-297	Sequence 297, App
26	2209	82.1	500	25	US-10-156-487A-6	Sequence 6, Appli
27	2185	81.2	431	1	PCT-US00-35260-36	Sequence 36, Appl
28	2185	81.2	431	23	US-09-912-935-36	Sequence 36, Appl
29	2185	81.2	431	25	US-10-168-365-36	Sequence 36, Appl
30	1296	48.2	528	27	US-60-242-679-1283	Sequence 1283, Ap
31	1295	48.1	435	27	US-60-327-731-14	Sequence 31, Appl
32	1295	48.1	499	1	PCT-US00-35260-31	Sequence 31, Appl
33	1295	48.1	499	23	US-09-912-935-31	Sequence 31, Appl
34	1295	48.1	499	25	US-10-168-365-31	Sequence 31, Appl
35	1295	48.1	529	1	PCT-US00-35260-28	Sequence 28, Appl
36	1295	48.1	529	1	PCT-US01-24031-189	Sequence 189, App
37	1295	48.1	529	1	PCT-US01-24031-200	Sequence 200, App
38	1295	48.1	529	1	PCT-US02-08253-189	Sequence 189, App
39	1295	48.1	529	1	PCT-US02-08253-200	Sequence 200, App
40	1295	48.1	529	1	PCT-US02-16639-4	Sequence 4, Appli
41	1295	48.1	529	23	US-09-912-935-28	Sequence 28, Appl
42	1295	48.1	529	23	US-09-912-935-40	Sequence 40, Appl
43	1295	48.1	529	23	US-09-918-715-189	Sequence 189, App
44	1295	48.1	529	23	US-09-918-715-200	Sequence 200, App
45	1295	48.1	529	25	US-10-156-487A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
PCT-US01-24031-230
Sequence 230, Application PC/TUS0124031

GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: PCT/US01/24031
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 230
LENGTH: 500
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-24031-230

Query Match 100.0%; Score 2691; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 7.9e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRGELWLLVLRRAALSPQAGHDEGPGGAAKAGTVRGWNNRARESPGHVSEPD 60
Db 1 MRGELWLLVLRRAALSPQAGHDEGPGGAAKAGTVRGWNNRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTLPDNRTRVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSQDLGGGTAMDTLPDNRTRVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
QY 121 IHTILSNTHRQASRVVLSFDPFPGHPLRQITATGGFIEMGDVTHRMMLTATQYVAPLMA 180
Db 121 IHTILSNTHRQASRVVLSFDPFPGHPLRQITATGGFIEMGDVTHRMMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYVFDNGTVFVQWQDHVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYVFDNGTVFVQWQDHVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
QY 301 LPTCLOHRSCDACMSDGLTFNCWCHVLRQCSGDFRYQEWMDYGCQAEAGRMCEDFQ 360
Db 301 LPTCLOHRSCDACMSDGLTFNCWCHVLRQCSGDFRYQEWMDYGCQAEAGRMCEDFQ 360
QY 361 DEDHDSASPTSFSPYDGLTITSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPTKGT 420
Db 361 DEDHDSASPTSFSPYDGLTITSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFTIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFTIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

RESULT 2
PCT-US02-08253-230
; Sequence 230, Application PC/TUS0208253
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: PCT/US02/08253
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-08253-230

```

```

Query Match 100.0%; Score 2691; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 7.9e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRGELWLLVLRRAALSPQAGHDEGPGGAAKAGTVRGWNNRARESPGHVSEPD 60
Db 1 MRGELWLLVLRRAALSPQAGHDEGPGGAAKAGTVRGWNNRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTLPDNRTRVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSQDLGGGTAMDTLPDNRTRVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120

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QY 121 IHTILSNTHRQASRVVLSFDPFPGHPLRQITATGGFIEMGDVTHRMMLTATQYVAPLMA 180
Db 121 IHTILSNTHRQASRVVLSFDPFPGHPLRQITATGGFIEMGDVTHRMMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYVFDNGTVFVQWQDHVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYVFDNGTVFVQWQDHVYLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
QY 301 LPTCLOHRSCDACMSDGLTFNCWCHVLRQCSGDFRYQEWMDYGCQAEAGRMCEDFQ 360
Db 301 LPTCLOHRSCDACMSDGLTFNCWCHVLRQCSGDFRYQEWMDYGCQAEAGRMCEDFQ 360
QY 361 DEDHDSASPTSFSPYDGLTITSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPTKGT 420
Db 361 DEDHDSASPTSFSPYDGLTITSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFTIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFTIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

```

```

RESULT 3
PCT-US02-29964-314
; Sequence 314, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aildong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Kyle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28

```

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 314
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-314

Query Match 100.0%; Score 2691; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 7.9e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGCTVGRGNRRARSPGHVSEPD 60
DB 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGCTVGRGNRRARSPGHVSEPD 60
QY 61 TQLSQDLGGGTAMDTPDNTRRVVVDNHNHYSYVSRLYGPPSPHRELWVDVAEANRSQVK 120
DB 61 TQLSQDLGGGTAMDTPDNTRRVVVDNHNHYSYVSRLYGPPSPHRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITITATGGFIEMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITITATGGFIEMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYVFDNGTFFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNPYSDNSTVYVFDNGTFFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPESRRRSIFEXHRIELDPKSVTMSAVEFTP 300
DB 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPESRRRSIFEXHRIELDPKSVTMSAVEFTP 300
QY 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360
QY 361 DEDHDSASPTSFSPYDGLTSSSLFIDSLTDDTKLNPYAGGDLQNNLSPKTKGT 420
DB 361 DEDHDSASPTSFSPYDGLTSSSLFIDSLTDDTKLNPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMPKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMPKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEAEQC 500
DB 481 YAEVPSGHEKEGFMEAEQC 500

RESULT 4
US-09-918-715-230
; Sequence 230, Application US/09918715
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-918-715-230

Query Match 100.0%; Score 2691; DB 23; Length 500;
Best Local Similarity 100.0%; Pred. No. 7.9e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGCTVGRGNRRARSPGHVSEPD 60
DB 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGCTVGRGNRRARSPGHVSEPD 60
QY 61 TQLSQDLGGGTAMDTPDNTRRVVVDNHNHYSYVSRLYGPPSPHRELWVDVAEANRSQVK 120
DB 61 TQLSQDLGGGTAMDTPDNTRRVVVDNHNHYSYVSRLYGPPSPHRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITITATGGFIEMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITITATGGFIEMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYVFDNGTFFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNPYSDNSTVYVFDNGTFFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPESRRRSIFEXHRIELDPKSVTMSAVEFTP 300
DB 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPESRRRSIFEXHRIELDPKSVTMSAVEFTP 300
QY 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSDITFNCWCHVLQRCSSGFDRYQEWMDYGCQAEGRMCEDFQ 360
QY 361 DEDHDSASPTSFSPYDGLTSSSLFIDSLTDDTKLNPYAGGDLQNNLSPKTKGT 420
DB 361 DEDHDSASPTSFSPYDGLTSSSLFIDSLTDDTKLNPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMPKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMPKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEAEQC 500
DB 481 YAEVPSGHEKEGFMEAEQC 500

RESULT 5

US-60-327-731-5

; Sequence 5, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-5

Query Match 100.0%; Score 2691; DB 27; Length 500;
Best Local Similarity 100.0%; Pred. No. 7.9e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLRARALSPQAGHDEGCGSGWAAGTGVGNRRRARESPGHVSEPR 60
DB 1 MRGELWLLVLVLRARALSPQAGHDEGCGSGWAAGTGVGNRRRARESPGHVSEPR 60
QY 61 TQSLDGLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
DB 61 TQSLDGLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVLSDFPFYGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVLSDFPFYGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYVDFNGTGVFWQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
DB 181 NFNPGYSDNSTVYVDFNGTGVFWQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMSEVETP 300
DB 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMSEVETP 300
QY 301 LPTCLQHRSCDACMSSDLTFNCSCHVLQRCSSGDFRYQEWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSSDLTFNCSCHVLQRCSSGDFRYQEWMDYGCQAEGRMCEDFQ 360
QY 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
DB 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEEAEOC 500
DB 481 YAEVPSGHEKEGFMEEAEOC 500

RESULT 6

US-60-327-731-15
; Sequence 15, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-15

Query Match 100.0%; Score 2691; DB 27; Length 500;
Best Local Similarity 100.0%; Pred. No. 7.9e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLRARALSPQAGHDEGCGSGWAAGTGVGNRRRARESPGHVSEPR 60
DB 1 MRGELWLLVLVLRARALSPQAGHDEGCGSGWAAGTGVGNRRRARESPGHVSEPR 60
QY 61 TQSLDGLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
DB 61 TQSLDGLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120

DB 61 TQSLDGLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVLSDFPFYGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVLSDFPFYGHPLRQITITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYVDFNGTGVFWQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
DB 181 NFNPGYSDNSTVYVDFNGTGVFWQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMSEVETP 300
DB 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMSEVETP 300
QY 301 LPTCLQHRSCDACMSSDLTFNCSCHVLQRCSSGDFRYQEWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSSDLTFNCSCHVLQRCSSGDFRYQEWMDYGCQAEGRMCEDFQ 360
QY 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
DB 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEEAEOC 500
DB 481 YAEVPSGHEKEGFMEEAEOC 500

RESULT 7

PCT-US02-29964-804
; Sequence 804, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Duntui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radolje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05


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; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 804
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-804

Query Match      100.0%; Score 2691; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 8,6e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
Db 28 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 87
Qy 61 TQLSODLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
Db 88 TQLSODLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 147
Qy 121 IHTILSNTHROASRVLSDFPFYGHPLRQITTIATGGFIFMGDV IHRMLTATQYVAPLMA 180
Db 148 IHTILSNTHROASRVLSDFPFYGHPLRQITTIATGGFIFMGDV IHRMLTATQYVAPLMA 207
Qy 181 NFNPGYSNNTVYVFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 208 NFNPGYSNNTVYVFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 267
Qy 241 SVPEISSSQHPVKTGLSDAEMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Db 268 SVPEISSSQHPVKTGLSDAEMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTP 327
Qy 301 LPTCLQHRSCDACMSDDLTFNCSCWCHVLQRCSSGFDRIYQEWMDYGCACAEAGRMCEDEQ 360
Db 328 LPTCLQHRSCDACMSDDLTFNCSCWCHVLQRCSSGFDRIYQEWMDYGCACAEAGRMCEDEQ 387
Qy 361 DEHDHSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Db 388 DEHDHSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 447
Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 448 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507
Qy 481 YAEVEPSGHEKEGFMEEAQC 500
Db 508 YAEVEPSGHEKEGFMEEAQC 527
```

RESULT 8

PCT-US02-29964-805

Sequence 805, Application PC/TUS0229964

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Ren, Feiyan

APPLICANT: Zhang, Jie

APPLICANT: Zhao, Qing A.

APPLICANT: Wang, Jian-Rui

APPLICANT: Xue, Aidong J.

APPLICANT: Wang, Dunrui

APPLICANT: Ghosh, Malabika

APPLICANT: Asundi, Vinod

APPLICANT: Wehrman, Tom

APPLICANT: Zhou, Ping

APPLICANT: Goodrich, Ryle W.

APPLICANT: Weng, Gezhi

APPLICANT: Haley-Vicente, Dana

APPLICANT: Drmanac, Radoje T

TITLE OF INVENTION: Novel Nucleic Acids and

TITLE OF INVENTION: Polypeptides

```
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 805
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-805

Query Match      100.0%; Score 2691; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 8,6e-265;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
Db 28 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 87
Qy 61 TQLSODLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
Db 88 TQLSODLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 147
Qy 121 IHTILSNTHROASRVLSDFPFYGHPLRQITTIATGGFIFMGDV IHRMLTATQYVAPLMA 180
Db 148 IHTILSNTHROASRVLSDFPFYGHPLRQITTIATGGFIFMGDV IHRMLTATQYVAPLMA 207
Qy 181 NFNPGYSNNTVYVFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 208 NFNPGYSNNTVYVFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 267
Qy 241 SVPEISSSQHPVKTGLSDAEMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTP 300
Db 268 SVPEISSSQHPVKTGLSDAEMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASAVEFTP 327
Qy 301 LPTCLQHRSCDACMSDDLTFNCSCWCHVLQRCSSGFDRIYQEWMDYGCACAEAGRMCEDEQ 360
Db 328 LPTCLQHRSCDACMSDDLTFNCSCWCHVLQRCSSGFDRIYQEWMDYGCACAEAGRMCEDEQ 387
Qy 361 DEHDHSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Db 388 DEHDHSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 447
Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 448 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507
Qy 481 YAEVEPSGHEKEGFMEEAQC 500
Db 508 YAEVEPSGHEKEGFMEEAQC 527
```

RESULT 9

US-60-327-731-3
 ; Sequence 3, Application US/60327731
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Malabika
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Ren, Feiyan
 ; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
 ; FILE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
 ; FILE REFERENCE: HYS-44
 ; CURRENT APPLICATION NUMBER: US/60/327,731
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 527
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; PCT-327-731-3

Query Match 100.0%; Score 2691; DB 27; Length 527;
 Best Local Similarity 100.0%; Pred. No. 8.6e-265;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRGELWLLVLR	AAARALSPQAGHDEPGSGWAAKGTVRGNRRARESPGHVSEPD	60
Db	28	MRGELWLLVLR	AAARALSPQAGHDEPGSGWAAKGTVRGNRRARESPGHVSEPD	87
QY	61	TQLSQDLGGGT	LTMDTLPDNRTRVVEDNHSYVSRLYGPPSEPHSRELWVDVAEANSQVK	120
Db	88	TQLSQDLGGGT	LTMDTLPDNRTRVVEDNHSYVSRLYGPPSEPHSRELWVDVAEANSQVK	147
QY	121	IHTILSNTHROASRV	LSFDFFPYGHPRLQITITATGGFIEMGDVTHRMLTATQYVAPLMA	180
Db	148	IHTILSNTHROASRV	LSFDFFPYGHPRLQITITATGGFIEMGDVTHRMLTATQYVAPLMA	207
QY	181	NFNPYSDNSTVYVD	NGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM	240
Db	208	NFNPYSDNSTVYVD	NGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM	267
QY	241	SVPEISSQHPVK	TGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP	300
Db	268	SVPEISSQHPVK	TGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP	327
QY	301	LPTCLQHRSCDAC	MSDLTFNCNCHVLRQCSGFDRIQEWMDYGCQAEGRMCEDFQ	360
Db	328	LPTCLQHRSCDAC	MSDLTFNCNCHVLRQCSGFDRIQEWMDYGCQAEGRMCEDFQ	387
QY	361	DEHDASPDTS	SPYDGLTTTSSSLFIDSLTDDTKLNPYAGGGLQNNLSPKTKGT	420
Db	388	DEHDASPDTS	SPYDGLTTTSSSLFIDSLTDDTKLNPYAGGGLQNNLSPKTKGT	447
QY	421	PVHLGTIVGIVL	AVALLVAAILAGIYINGHPTNAALFFIERRPHHPAMKFRSHPDHST	480
Db	448	PVHLGTIVGIVL	AVALLVAAILAGIYINGHPTNAALFFIERRPHHPAMKFRSHPDHST	507
QY	481	YAEVPSGHEKEG	FMEAEQC 500	
Db	508	YAEVPSGHEKEG	FMEAEQC 527	

RESULT 10

PCT-US01-24031-179
 ; Sequence 179, Application PC/TUS0124031
 ; GENERAL INFORMATION:
 ; APPLICANT: Brad St. Croix
 ; APPLICANT: Bert Vogelstein

; APPLICANT: Kenneth Kinzler
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 ; FILE REFERENCE: 1107.00134
 ; CURRENT APPLICATION NUMBER: PCT/US01/24031
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: 60/222,599
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: 60/224,360
 ; PRIOR FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: 60/282,850
 ; PRIOR FILING DATE: 2000-04-11
 ; NUMBER OF SEQ ID NOS: 358
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 179
 ; LENGTH: 1002
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PCT-US01-24031-179

Query Match 100.0%; Score 2691; DB 1; Length 1002;
 Best Local Similarity 100.0%; Pred. No. 2.4e-264;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRGELWLLVLR	AAARALSPQAGHDEPGSGWAAKGTVRGNRRARESPGHVSEPD	60
Db	503	MRGELWLLVLR	AAARALSPQAGHDEPGSGWAAKGTVRGNRRARESPGHVSEPD	562
QY	61	TQLSQDLGGGT	LTMDTLPDNRTRVVEDNHSYVSRLYGPPSEPHSRELWVDVAEANSQVK	120
Db	563	TQLSQDLGGGT	LTMDTLPDNRTRVVEDNHSYVSRLYGPPSEPHSRELWVDVAEANSQVK	622
QY	121	IHTILSNTHROASRV	LSFDFFPYGHPRLQITITATGGFIEMGDVTHRMLTATQYVAPLMA	180
Db	623	IHTILSNTHROASRV	LSFDFFPYGHPRLQITITATGGFIEMGDVTHRMLTATQYVAPLMA	682
QY	181	NFNPYSDNSTVYVD	NGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM	240
Db	683	NFNPYSDNSTVYVD	NGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM	742
QY	241	SVPEISSQHPVK	TGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP	300
Db	743	SVPEISSQHPVK	TGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP	802
QY	301	LPTCLQHRSCDAC	MSDLTFNCNCHVLRQCSGFDRIQEWMDYGCQAEGRMCEDFQ	360
Db	803	LPTCLQHRSCDAC	MSDLTFNCNCHVLRQCSGFDRIQEWMDYGCQAEGRMCEDFQ	862
QY	361	DEHDASPDTS	SPYDGLTTTSSSLFIDSLTDDTKLNPYAGGGLQNNLSPKTKGT	420
Db	863	DEHDASPDTS	SPYDGLTTTSSSLFIDSLTDDTKLNPYAGGGLQNNLSPKTKGT	922
QY	421	PVHLGTIVGIVL	AVALLVAAILAGIYINGHPTNAALFFIERRPHHPAMKFRSHPDHST	480
Db	923	PVHLGTIVGIVL	AVALLVAAILAGIYINGHPTNAALFFIERRPHHPAMKFRSHPDHST	982
QY	481	YAEVPSGHEKEG	FMEAEQC 500	
Db	983	YAEVPSGHEKEG	FMEAEQC 1002	

RESULT 11
 PCT-US02-08253-179
 ; Sequence 179, Application PC/TUS0208253
 ; GENERAL INFORMATION:
 ; APPLICANT: Carson-Walter, Eleanor
 ; APPLICANT: St. Croix, Brad
 ; APPLICANT: Vogelstein, Bert
 ; APPLICANT: Kinzler, Kenneth
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 ; FILE REFERENCE: 1107.00179
 ; CURRENT APPLICATION NUMBER: PCT/US02/08253
 ; CURRENT FILING DATE: 2002-04-10
 ; PRIOR APPLICATION NUMBER: 60/282,850

; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-08253-179

Query Match 100.0%; Score 2691; DB 1; Length 1002;
Best Local Similarity 100.0%; Pred. No. 2.4e-264;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
DB 503 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 562
QY 61 TQSLDGLGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEHRELWVDVAEANRSQVK 120
DB 563 TQSLDGLGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEHRELWVDVAEANRSQVK 622
QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
DB 623 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 682
QY 181 NFNPGYSDNSTVYVDFNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 683 NFNPGYSDNSTVYVDFNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 742
QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
DB 743 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 802
QY 301 LPTCLQHRSCDACMSDGLTTFNCSWCHVLQRCSSGDFRYQEWMDYGCQAEGRMCEDFQ 360
DB 803 LPTCLQHRSCDACMSDGLTTFNCSWCHVLQRCSSGDFRYQEWMDYGCQAEGRMCEDFQ 862
QY 361 DEDHDSASPTSFSPYDGLTTFSSSLFIDSLTDEDDTKLNPYAGDGLQNNLSPKTKGT 420
DB 863 DEDHDSASPTSFSPYDGLTTFSSSLFIDSLTDEDDTKLNPYAGDGLQNNLSPKTKGT 922
QY 421 PVHLGTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 480
DB 923 PVHLGTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 982
QY 481 YAEVPSGHEKEGFMEAEQC 500
DB 983 YAEVPSGHEKEGFMEAEQC 1002

RESULT 12
US-09-918-715-179
; Sequence 179, Application US/09918715
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT FILING DATE: 2001-08-01
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-179
Query Match 100.0%; Score 2691; DB 23; Length 1002;
Best Local Similarity 100.0%; Pred. No. 2.4e-264;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
DB 503 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 562
QY 61 TQSLDGLGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEHRELWVDVAEANRSQVK 120
DB 563 TQSLDGLGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPSEHRELWVDVAEANRSQVK 622
QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
DB 623 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 682
QY 181 NFNPGYSDNSTVYVDFNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 683 NFNPGYSDNSTVYVDFNGTGVVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 742
QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
DB 743 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 802
QY 301 LPTCLQHRSCDACMSDGLTTFNCSWCHVLQRCSSGDFRYQEWMDYGCQAEGRMCEDFQ 360
DB 803 LPTCLQHRSCDACMSDGLTTFNCSWCHVLQRCSSGDFRYQEWMDYGCQAEGRMCEDFQ 862
QY 361 DEDHDSASPTSFSPYDGLTTFSSSLFIDSLTDEDDTKLNPYAGDGLQNNLSPKTKGT 420
DB 863 DEDHDSASPTSFSPYDGLTTFSSSLFIDSLTDEDDTKLNPYAGDGLQNNLSPKTKGT 922
QY 421 PVHLGTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 480
DB 923 PVHLGTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 982
QY 481 YAEVPSGHEKEGFMEAEQC 500
DB 983 YAEVPSGHEKEGFMEAEQC 1002
RESULT 13
PCT-US02-29964-315
; Sequence 315, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: pt_FGenes Version 6.0
; SEQ ID NO 315
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-315

Query Match 96.9%; Score 2607; DB 1; Length 488;
Best Local Similarity 97.6%; Pred. No. 2.9e-256;
Matches 488; Conservative 0; Mismatches 0; Indels 12; Gaps 1;
QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTPDNTRRVVDENHNSYYVRLYGPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSQDLGGGTAMDTPDNTRRVVDENHNSYYVRLYGPSEPHSRELWVDVAEANSQVK 120
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
Db 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGAQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNPYAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTVIGVILVAVLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 409 PVHLGTVIGVILVAVLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEAEQC 500
Db 469 YAEVPSGHEKEGFMEAEQC 488

RESULT 14
US-60-327-731-10
; Sequence 10, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan

; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 488
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-10

Query Match 96.9%; Score 2607; DB 27; Length 488;
Best Local Similarity 97.6%; Pred. No. 2.9e-256;
Matches 488; Conservative 0; Mismatches 0; Indels 12; Gaps 1;
QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTPDNTRRVVDENHNSYYVRLYGPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSQDLGGGTAMDTPDNTRRVVDENHNSYYVRLYGPSEPHSRELWVDVAEANSQVK 120
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
Db 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSSDLTFCNSWCHVLQRCSSGFDRYQEWMDYGAQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNPYAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTVIGVILVAVLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 409 PVHLGTVIGVILVAVLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMEAEQC 500
Db 469 YAEVPSGHEKEGFMEAEQC 488

RESULT 15
US-60-327-731-8
; Sequence 8, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017

; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 482
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-8

Query Match 96.8%; Score 2604; DB 27; Length 482;
Best Local Similarity 100.0%; Pred. No. 5.7e-256;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTLP 78
Db 1 LSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTLP 60

QY 79 DNRTRVEDNHSYYVSRLYGSEPHSRRLWVDAEANKRSQVKIHTILSNTHRQASRVVLS 138
Db 61 DNRTRVEDNHSYYVSRLYGSEPHSRRLWVDAEANKRSQVKIHTILSNTHRQASRVVLS 120

QY 139 FDFPYGHPRLQITTIATGGFIFMGDV IHRMLTATQYVAPLMANFNPGYSDNSTVVFYDNG 198
Db 121 FDFPYGHPRLQITTIATGGFIFMGDV IHRMLTATQYVAPLMANFNPGYSDNSTVVFYDNG 180

QY 199 TVFVQWHDVYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGSD 258
Db 181 TVFVQWHDVYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGSD 240

QY 259 AFMILNPSPDVPESRRRIFVYHRIELDPISKVTSMSAVEFTPLPTCLOHRSCDACMSSDL 318
Db 241 AFMILNPSPDVPESRRRIFVYHRIELDPISKVTSMSAVEFTPLPTCLOHRSCDACMSSDL 300

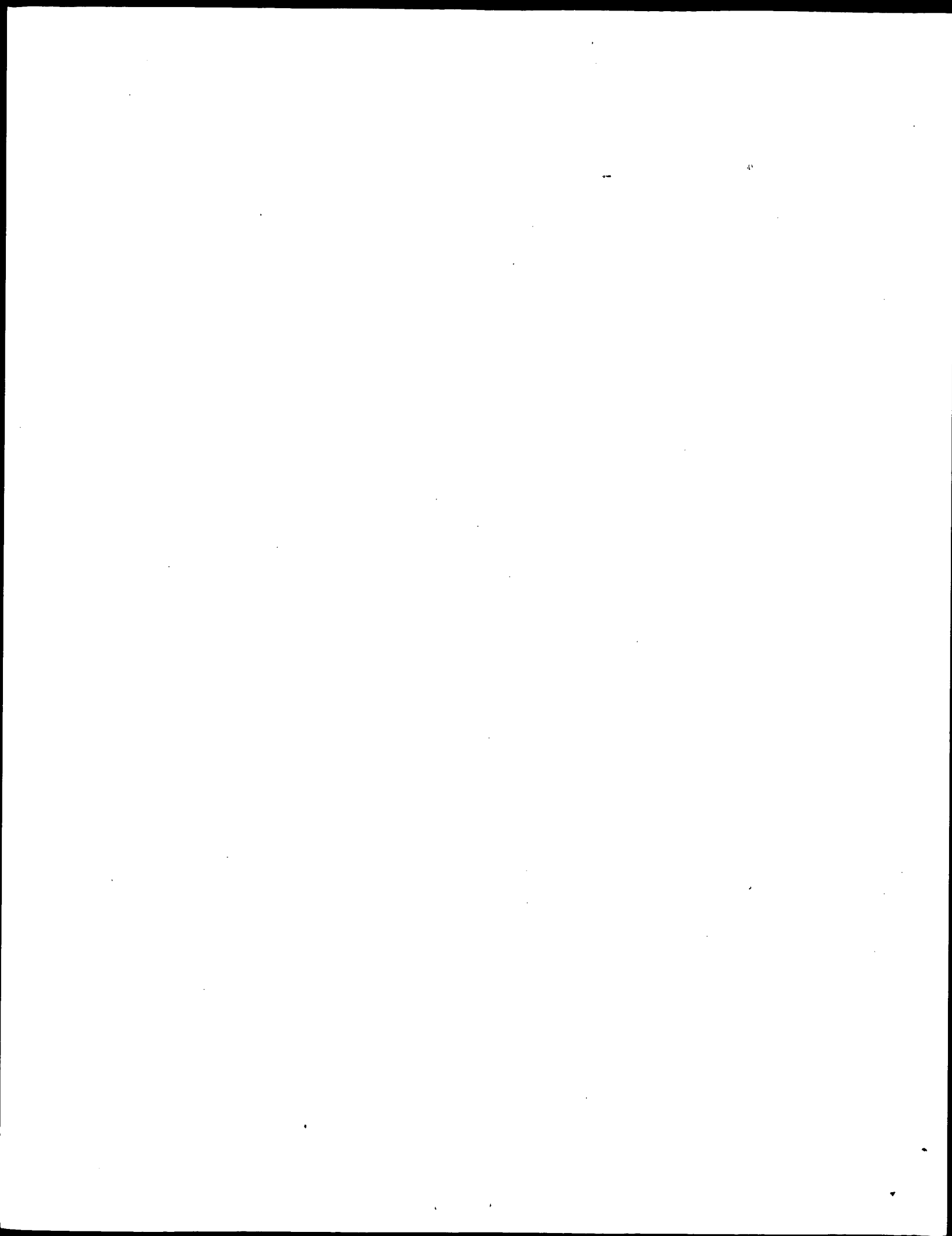
QY 319 TENCSCWHLQRCSSGFDRYRQWMDYCAQAEGRMCEDFQDEHDSASPDTSFSPYDG 378
Db 301 TENCSCWHLQRCSSGFDRYRQWMDYCAQAEGRMCEDFQDEHDSASPDTSFSPYDG 360

QY 379 DLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTIVGIVLAVLLVA 438
Db 361 DLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGTPVHLGTIVGIVLAVLLVA 420

QY 439 AIIAGIYINGHPTNNAALFFIERPHHPAMKFRSHDPHSTYAEVPSGHEKEGFMEEAE 498
Db 421 AIIAGIYINGHPTNNAALFFIERPHHPAMKFRSHDPHSTYAEVPSGHEKEGFMEEAE 480

QY 499 QC 500
Db 481 QC 482

Search completed: April 22, 2003, 16:14:10
Job time : 326 secs



GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:07:15 ; Search time 36 Seconds
(without alignments)
2191.561 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELWLLVLRRAARALS.....YAEVPSGHEKEGFMEAEQC 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 718614 seqs, 157792391 residues

Total number of hits satisfying chosen parameters: 718614

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending_Patents_AA_New:*
- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pcp:**
 - 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pcp:**
 - 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pcp:**
 - 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pcp:**
 - 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pcp:**
 - 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pcp:**
 - 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pcp:**

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2691	100.0	500	6	US-10-266-252-5	Sequence 5, Appli
2	2691	100.0	500	6	US-10-266-252-15	Sequence 15, Appl
3	2691	100.0	500	7	US-60-453-135-13631	Sequence 13631, A
4	2691	100.0	500	7	US-60-453-050-13631	Sequence 13631, A
5	2691	100.0	527	6	US-10-266-252-3	Sequence 3, Appli
6	2607	96.9	488	6	US-10-266-252-10	Sequence 10, Appl
7	2604	96.8	482	6	US-10-266-252-8	Sequence 8, Appli
8	2520	93.6	470	6	US-10-266-252-12	Sequence 12, Appl
9	2302	85.5	427	7	US-60-453-135-13630	Sequence 13630, A
10	2302	85.5	427	7	US-60-453-050-13630	Sequence 13630, A
11	2007	74.6	400	6	US-10-218-140-5790	Sequence 5790, Ap
12	1295	48.1	435	6	US-10-266-252-14	Sequence 14, Appl
13	1294	48.1	529	6	US-10-123-923A-472	Sequence 472, App
14	1294	48.1	529	6	US-10-205-892-472	Sequence 472, App
15	1294	48.1	529	6	US-10-174-575-472	Sequence 472, App
16	1294	48.1	529	6	US-10-174-575A-472	Sequence 472, App
17	1294	48.1	529	6	US-10-187-755-472	Sequence 472, App
18	1294	48.1	529	6	US-10-187-749-472	Sequence 472, App
19	1294	48.1	529	6	US-10-199-672-472	Sequence 472, App
20	1294	48.1	529	6	US-10-194-486-472	Sequence 472, App
21	1275.5	47.4	530	1	PCT-US02-34451-12	Sequence 12, Appl
22	1275.5	47.4	530	6	US-10-281-478-12	Sequence 12, Appl
23	1150	42.7	379	7	US-60-452-680-20245	Sequence 20245, A
24	697	25.9	146	6	US-10-264-237-2453	Sequence 2453, Ap
25	682.5	25.4	290	6	US-10-218-140-526	Sequence 526, App
26	115.5	4.3	1265	5	US-09-724-676-82419	Sequence 82419, A

ALIGNMENTS

RESULT 1

US-10-266-252-5

: Sequence 5, Application US/10266252

: GENERAL INFORMATION:

: APPLICANT: Ghosh, Malabika

: APPLICANT: Tang, Y. Tom

: TITLE OF INVENTION: Ren, Feiyan

: TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like

: FILE REFERENCE: HVS-44A

: CURRENT APPLICATION NUMBER: US/10/266,252

: CURRENT FILING DATE: 2002-10-07

: PRIOR APPLICATION NUMBER: 60/327,731

: PRIOR FILING DATE: 2001-10-05

: PRIOR APPLICATION NUMBER: PCT/US00/35017

: PRIOR FILING DATE: 2000-12-22

: PRIOR APPLICATION NUMBER: 09/552,317

: PRIOR FILING DATE: 2000-04-25

: PRIOR APPLICATION NUMBER: 09/488,725

: NUMBER OF SEQ ID NOS: 15

: SOFTWARE: PatentIn version 3.1

: SEQ ID NO 5

: LENGTH: 500

: TYPE: PRT

: ORGANISM: homo sapiens

: US-10-266-252-5

Query Match 100.0%; Score 2691; DB 6; Length 500;

Best Local Similarity 100.0%; Pred. No. 1.8e+226;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRGELWLLVLRRAARALSPPGAGHDEGPGSGWAAGTVRGWNRRAARESPGHVSEPD	60
Db	1	MRGELWLLVLRRAARALSPPGAGHDEGPGSGWAAGTVRGWNRRAARESPGHVSEPD	60
Qy	61	TOLSQDLGGGTAMDTLPDNRTRVVDNHNHYSYVRLXGPPSPHRELWVDVAEANSQVK	120
Db	61	TOLSQDLGGGTAMDTLPDNRTRVVDNHNHYSYVRLXGPPSPHRELWVDVAEANSQVK	120
Qy	121	IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIEMGDVTHRLMTATQVAPLMA	180
Db	121	IHTILSNTHROASRVLSFDFPFYGHPLRQITATGGFIEMGDVTHRLMTATQVAPLMA	180
Qy	181	NFNPGYSDNSVWYFDNGTVFWQWDHVLVLOGWEDKSGSFTFQAALHHDGRIVFAYKEIPM	240
Db	181	NFNPGYSDNSVWYFDNGTVFWQWDHVLVLOGWEDKSGSFTFQAALHHDGRIVFAYKEIPM	240
Qy	241	SVPEISSQHPVKTLGLSDAFMILNPSDPVPSRRRSIFEXHRIELDPSPKSVTSMAVEFTP	300

Db 241 SVPEISSQHPVKTKLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSSGFDYRQEMNDYGCQAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSSGFDYRQEMNDYGCQAQAEGRMCEDFQ 360
QY 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGMEAEQC 500
Db 481 YAEVPSGHEKEGMEAEQC 500

RESULT 2

US-10-266-252-15
; Sequence 15, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Felyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HVS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-15

Query Match 100.0%; Score 2691; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.8e-226;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPR 60
Db 1 MRGELWLLVLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPR 60
QY 61 TQSDQLGGGTILAMDTLPDNRTRVVDNHSYVSRLYGSPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSDQLGGGTILAMDTLPDNRTRVVDNHSYVSRLYGSPSEPHSRELWVDVAEANSQVK 120
QY 121 IHTILSNTHROASRVVLSFDFFPGHPLRQITATGGIFPMGDVIRHMLTATQYVAPLMA 180
Db 121 IHTILSNTHROASRVVLSFDFFPGHPLRQITATGGIFPMGDVIRHMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTKLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
Db 241 SVPEISSQHPVKTKLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSSGFDYRQEMNDYGCQAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSSGFDYRQEMNDYGCQAQAEGRMCEDFQ 360
QY 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGMEAEQC 500
Db 481 YAEVPSGHEKEGMEAEQC 500

Db 301 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSSGFDYRQEMNDYGCQAQAEGRMCEDFQ 360
QY 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGMEAEQC 500
Db 481 YAEVPSGHEKEGMEAEQC 500

RESULT 3

US-60-453-135-13631
; Sequence 13631, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: TAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13631
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13631

Query Match 100.0%; Score 2691; DB 7; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.8e-226;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPR 60
Db 1 MRGELWLLVLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPR 60
QY 61 TQSDQLGGGTILAMDTLPDNRTRVVDNHSYVSRLYGSPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSDQLGGGTILAMDTLPDNRTRVVDNHSYVSRLYGSPSEPHSRELWVDVAEANSQVK 120
QY 121 IHTILSNTHROASRVVLSFDFFPGHPLRQITATGGIFPMGDVIRHMLTATQYVAPLMA 180
Db 121 IHTILSNTHROASRVVLSFDFFPGHPLRQITATGGIFPMGDVIRHMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTKLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
Db 241 SVPEISSQHPVKTKLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSSGFDYRQEMNDYGCQAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSSGFDYRQEMNDYGCQAQAEGRMCEDFQ 360
QY 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEHDASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGMEAEQC 500
Db 481 YAEVPSGHEKEGMEAEQC 500

Db 481 YAEVPSGHEKEGMEAEQC 500

RESULT 4

US-60-453-050-13631
; Sequence 13631, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/60/453.050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13631
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13631

Query Match 100.0%; Score 2691; DB 7; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.8e-226;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGCTVGRWNNRRARESPGHVSEPD 60
|||||
Db 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGCTVGRWNNRRARESPGHVSEPD 60
|||||

QY 61 TQSDQLGGGTLMADTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
|||||
Db 61 TQSDQLGGGTLMADTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
|||||

QY 121 IHTILSNTHRQASRVVLSDFPFYGHPLRQITATGGTFPMGDVIHRMLTATQYVAPLMA 180
|||||
Db 121 IHTILSNTHRQASRVVLSDFPFYGHPLRQITATGGTFPMGDVIHRMLTATQYVAPLMA 180
|||||

QY 181 NENPGYSDNSTVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
|||||
Db 181 NENPGYSDNSTVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
|||||

QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASVEFTP 300
|||||
Db 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASVEFTP 300
|||||

QY 301 LPTCLQHRSCDACMSDLTFNCSWCHVLRQCSGFDRYRQEMWDYGCQAEGRMCEDFQ 360
|||||
Db 301 LPTCLQHRSCDACMSDLTFNCSWCHVLRQCSGFDRYRQEMWDYGCQAEGRMCEDFQ 360
|||||

QY 361 DEHDHSDASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLONNLSPKTKGT 420
|||||
Db 361 DEHDHSDASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLONNLSPKTKGT 420
|||||

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
|||||
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
|||||

QY 481 YAEVPSGHEKEGMEAEQC 500
|||||
Db 481 YAEVPSGHEKEGMEAEQC 500
|||||

RESULT 5

US-10-266-252-3
; Sequence 3, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: Polypeptides and Polynucleotides and Therapeutic Uses Thereof

; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 527
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-3

Query Match 100.0%; Score 2691; DB 6; Length 527;
Best Local Similarity 100.0%; Pred. No. 1.9e-226;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGCTVGRWNNRRARESPGHVSEPD 60
|||||
Db 28 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGCTVGRWNNRRARESPGHVSEPD 87
|||||

QY 61 TQSDQLGGGTLMADTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
|||||
Db 88 TQSDQLGGGTLMADTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 147
|||||

QY 121 IHTILSNTHRQASRVVLSDFPFYGHPLRQITATGGTFPMGDVIHRMLTATQYVAPLMA 180
|||||
Db 148 IHTILSNTHRQASRVVLSDFPFYGHPLRQITATGGTFPMGDVIHRMLTATQYVAPLMA 207
|||||

QY 181 NENPGYSDNSTVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
|||||
Db 208 NENPGYSDNSTVYFDNGTVFVQWDHVVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 267
|||||

QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASVEFTP 300
|||||
Db 268 SVPEISSQHVPKVTGLSDAFMILNPSDPVPESRRRSIFEYHRIELDPKVTSMASVEFTP 327
|||||

QY 301 LPTCLQHRSCDACMSDLTFNCSWCHVLRQCSGFDRYRQEMWDYGCQAEGRMCEDFQ 360
|||||
Db 328 LPTCLQHRSCDACMSDLTFNCSWCHVLRQCSGFDRYRQEMWDYGCQAEGRMCEDFQ 387
|||||

QY 361 DEHDHSDASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLONNLSPKTKGT 420
|||||
Db 388 DEHDHSDASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGDGLONNLSPKTKGT 447
|||||

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
|||||
Db 448 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507
|||||

QY 481 YAEVPSGHEKEGMEAEQC 500
|||||
Db 508 YAEVPSGHEKEGMEAEQC 527
|||||

RESULT 6

US-10-266-252-10
; Sequence 10, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 488
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-10

Query Match 96.9%; Score 2607; DB 6; Length 488;
Best Local Similarity 97.6%; Pred. No. 3.7e-219;
Matches 488; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60

QY 61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHRSRELWVDVAEANRSQVK 120
Db 61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYVSRLYGSPHRSRELWVDVAEANRSQVK 120

QY 121 IHTILSNTHRQASRVVLSFDPFFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180
Db 121 IHTILSNTHRQASRVVLSFDPFFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMA 180

QY 181 NFNPYSDNSTVYFDNGTTFVQWQDHVYLOGWEDKGSFTFQAAALHHDGRIVFAKKEIPM 240
Db 181 NFNPYSDNSTVYFDNGTTFVQWQDHVYLOGWEDKGSFTFQAAALHHDGRIVFAKKEIPM 240

QY 241 SVPEISSSOHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300
Db 241 SVPEISSSOHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTP 300

QY 301 LPTCLQHRSCDACMSDITFNCWCHVLRQCSGFDYRQEMDYGCAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSDITFNCWCHVLRQCSGFDYRQEMDYGCAQAEGRMCEDFQ 360

QY 361 DEHDHSDPSTSFSDYDGLTSSSLFIDSLTTE-----GLQNNLSFKTKGT 420
Db 361 DEHDHSDPSTSFSDYDGLTSSSLFIDSLTTE-----GLQNNLSFKTKGT 408

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHST 480
Db 409 PVHLGTIVGIVLAVLLVAAILAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHST 468

QY 481 YAEVPSGHEKEGMEAEQC 500
Db 469 YAEVPSGHEKEGMEAEQC 488

RESULT 7
US-10-266-252-8
; Sequence 8, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 482
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-8

Query Match 96.8%; Score 2604; DB 6; Length 482;
Best Local Similarity 100.0%; Pred. No. 6.7e-219;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSODLGGGTLAMDTLP 78
Db 1 LSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPDRTQLSODLGGGTLAMDTLP 60

QY 79 DNRTRVVEDNHSYVSRLYGSPHRSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLS 138
Db 61 DNRTRVVEDNHSYVSRLYGSPHRSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLS 120

QY 139 FDPFFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPNPGYSDNSTVYFDNG 198
Db 121 FDPFFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMAFNPNPGYSDNSTVYFDNG 180

QY 199 TVFVQWQDHVYLOGWEDKGSFTFQAAALHHDGRIVFAKKEIPMSVPEISSOHPVKTGLSD 258
Db 181 TVFVQWQDHVYLOGWEDKGSFTFQAAALHHDGRIVFAKKEIPMSVPEISSOHPVKTGLSD 240

QY 259 AFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTPCLQHRSCDACMSDDL 318
Db 241 AFMLNPSDPVPSRRRSIFEYHRIELDPKVTSMASVEFTPCLQHRSCDACMSDDL 300

QY 319 TFNCWCHVLRQCSGFDYRQEMDYGCAQAEGRMCEDFQDEHSDASPTSFSPYDG 378
Db 301 TFNCWCHVLRQCSGFDYRQEMDYGCAQAEGRMCEDFQDEHSDASPTSFSPYDG 360

QY 379 DLTTSSSLFIDSLTTEDDTKLNPYAGGDLQNNLSFKTKGTPVHLGTIVGIVLAVLLVA 438
Db 361 DLTTSSSLFIDSLTTEDDTKLNPYAGGDLQNNLSFKTKGTPVHLGTIVGIVLAVLLVA 420

QY 439 AITLAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEGMEAE 498
Db 421 AITLAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEGMEAE 480

QY 499 QC 500
Db 481 QC 482

RESULT 8
US-10-266-252-12
; Sequence 12, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 12
; LENGTH: 470
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-12

Query Match      93.6%; Score 2520; DB 6; Length 470;
Best Local Similarity 97.5%; Pred. No. 1.4e-211;
Matches 470; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY 19 LSPQAGHDEGPGSGWAAGKTVRGWNRARRSPGHVSEPDRTQSLDGGTTLAMDPLP 78
DB 1 LSPQAGHDEGPGSGWAAGKTVRGWNRARRSPGHVSEPDRTQSLDGGTTLAMDPLP 60

QY 79 DNRTRVEDNHHYYSRSLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROASRVVLS 138
DB 61 DNRTRVEDNHHYYSRSLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROASRVVLS 120

QY 139 FDFPFYGHPLROITITATGGFIFMGDVIIHRMLTATQYVAPLMANFPGYSDNSTVYFONG 198
DB 121 FDFPFYGHPLROITITATGGFIFMGDVIIHRMLTATQYVAPLMANFPGYSDNSTVYFONG 180

QY 199 TVFVQWMDHVYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSD 258
DB 181 TVFVQWMDHVYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSD 240

QY 259 AFMILNPSDPVESRRRSIFEHRIELDPKSVTSMASVEFTPLPTCLOHRSDDACMSDDL 318
DB 241 AFMILNPSDPVESRRRSIFEHRIELDPKSVTSMASVEFTPLPTCLOHRSDDACMSDDL 300

QY 319 TFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQDEHDHDSASPDTSF 378
DB 301 TFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQDEHDHDSASPDTSF 360

QY 379 DLTTSSSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTIVGLVLA 438
DB 361 DLTTSSSLFIDSLTTE-----GLQNNLSPKTKGTPVHLGTIVGLVLA 408

QY 439 AILAGIYINGHTPSNAALFFIERRPHHPAMPKFRSHPDHSTYAEVPSGHEKEGMEAE 498
DB 409 AILAGIYINGHTPSNAALFFIERRPHHPAMPKFRSHPDHSTYAEVPSGHEKEGMEAE 468

QY 499 QC 500
DB 469 QC 470

RESULT 9
US-60-453-135-13630
; Sequence 13630, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: JAKUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13630
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13630

Query Match      85.5%; Score 2302; DB 7; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.4e-192;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 MDLTPDNRTRVEDNHHYYSRSLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROAS 133
DB 1 MDLTPDNRTRVEDNHHYYSRSLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROAS 60

QY 134 RVVLSDFPFYGHPLROITITATGGFIFMGDVIIHRMLTATQYVAPLMANFPGYSDNSTV 193
DB 61 RVVLSDFPFYGHPLROITITATGGFIFMGDVIIHRMLTATQYVAPLMANFPGYSDNSTV 120

QY 194 YFDNGTVFVQWMDHVYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVK 253
DB 121 YFDNGTVFVQWMDHVYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVK 180

QY 254 TGLSDAFMILNPSDPVESRRRSIFEHRIELDPKSVTSMASVEFTPLPTCLOHRSDDAC 313
DB 181 TGLSDAFMILNPSDPVESRRRSIFEHRIELDPKSVTSMASVEFTPLPTCLOHRSDDAC 240

QY 314 MSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQDEHDHDSASPDTSF 373
DB 241 MSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQDEHDHDSASPDTSF 300

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QY 134 RVVLSDFPFYGHPLROITITATGGFIFMGDVIIHRMLTATQYVAPLMANFPGYSDNSTV 193
DB 61 RVVLSDFPFYGHPLROITITATGGFIFMGDVIIHRMLTATQYVAPLMANFPGYSDNSTV 120

QY 194 YFDNGTVFVQWMDHVYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVK 253
DB 121 YFDNGTVFVQWMDHVYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVK 180

QY 254 TGLSDAFMILNPSDPVESRRRSIFEHRIELDPKSVTSMASVEFTPLPTCLOHRSDDAC 313
DB 181 TGLSDAFMILNPSDPVESRRRSIFEHRIELDPKSVTSMASVEFTPLPTCLOHRSDDAC 240

QY 314 MSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQDEHDHDSASPDTSF 373
DB 241 MSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQDEHDHDSASPDTSF 300

QY 374 SPYDGDLTSSSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTIVGLVLA 433
DB 301 SPYDGDLTSSSLFIDSLTTEDDTKLNPYAGDGLQNNLSPKTKGTPVHLGTIVGLVLA 360

QY 434 VLLVAAIILAGIYINGHTPSNAALFFIERRPHHPAMPKFRSHPDHSTYAEVPSGHEKEG 493
DB 361 VLLVAAIILAGIYINGHTPSNAALFFIERRPHHPAMPKFRSHPDHSTYAEVPSGHEKEG 420

QY 494 FMEAEQC 500
DB 421 FMEAEQC 427

RESULT 10
US-60-453-050-13630
; Sequence 13630, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13630
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13630

Query Match      85.5%; Score 2302; DB 7; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.4e-192;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 MDLTPDNRTRVEDNHHYYSRSLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROAS 133
DB 1 MDLTPDNRTRVEDNHHYYSRSLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROAS 60

QY 134 RVVLSDFPFYGHPLROITITATGGFIFMGDVIIHRMLTATQYVAPLMANFPGYSDNSTV 193
DB 61 RVVLSDFPFYGHPLROITITATGGFIFMGDVIIHRMLTATQYVAPLMANFPGYSDNSTV 120

QY 194 YFDNGTVFVQWMDHVYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVK 253
DB 121 YFDNGTVFVQWMDHVYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSSQHPVK 180

QY 254 TGLSDAFMILNPSDPVESRRRSIFEHRIELDPKSVTSMASVEFTPLPTCLOHRSDDAC 313
DB 181 TGLSDAFMILNPSDPVESRRRSIFEHRIELDPKSVTSMASVEFTPLPTCLOHRSDDAC 240

QY 314 MSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQDEHDHDSASPDTSF 373
DB 241 MSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQDEHDHDSASPDTSF 300

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QY 374 SPYDGLTTSSSLFIDSLTETDTHKLNYPAGDGLQNNLSPKTKGTVPVHLGTIVGIVLA 433
Db 301 SPYDGLTTSSSLFIDSLTETDTHKLNYPAGDGLQNNLSPKTKGTVPVHLGTIVGIVLA 360
QY 434 VLLVAAILLAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHSTYAEVPEPSGHEKEG 493
Db 361 VLLVAAILLAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHSTYAEVPEPSGHEKEG 420
QY 494 FMEAEQC 500
Db 421 FMEAEQC 427

RESULT 11
US-10-218-140-5790
; Sequence 5790, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curator Version 1.0
; SEQ ID NO 5790
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
; OTHER INFORMATION: "Xaa" = "Any Amino Acid"
US-10-218-140-5790

Query Match 74.6%; Score 2007; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 7.8e-167;
Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTVRGWNRRAARESPGHVSEPD 60
Db 29 MRGELWLLVLRRAARALSPQAGHDEGPGSGWAAGTVRGWNRRAARESPGHVSEPD 88
QY 61 TQSLDGLGGTFLAMDTLPDNRTRVEDNHSYVSRLYGSEPHSRELWVDVAEANRSQVK 120
Db 89 TQSLDGLGGTFLAMDTLPDNRTRVEDNHSYVSRLYGSEPHSRELWVDVAEANRSQVK 148
QY 121 IHTLSNTHRCASRVLSDFEPFYGHPLRQITATGTFIMGDVHRLMTATQYVAPLMA 180
Db 149 IHTLSNTHRCASRVLSDFEPFYGHPLRQITATGTFIMGDVHRLMTATQYVAPLMA 208
QY 181 NFNPYSDNNTVYFDNGTVFVQWQDHVYLQGWEDKGSFTFQAAALHHDGRIVEFYAYKEIPM 240
Db 209 NFNPYSDNNTVYFDNGTVFVQWQDHVYLQGWEDKGSFTFQAAALHHDGRIVEFYAYKEIPM 268
QY 241 SVPEISSQHPVKTGLSDAFMLNPSFDVPSRRSIFFYHRIELDPKSVTMSAVEFT 300
Db 269 SVPEISSQHPVKTGLSDAFMLNPSFDVPSRRSIFFYHRIELDPKSVTMSAVEFT 328
QY 301 LPTCLOHRSQDACMSSDLTFNCMCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 360
Db 329 LPTCLOHRSQDACMSSDLTFNCMCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQ 388
QY 361 DEDHDSASPD 371

Db 389 DEDHDSASPD 399

RESULT 12
US-10-266-252-14
; Sequence 14, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Rang, Y. Tom
; APPLICANT: Ren, Felyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 435
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-14

Query Match 48.1%; Score 1295; DB 6; Length 435;

Best Local Similarity 57.3%; Pred. No. 1.5e-104;

Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVED-NHSYVSRLYGSEPHSRELWVDVAEANRSQVKIHTLSNTHR 130
Db 1 LLLDGDQDNNQTIEDTDHNYIISRIYSPDSASRLWYINIDQMEKDKVKIHGILSNTHR 60
QY 131 QASRVVLSDFEPFYGHPLRQITATGTFIMGDVHRLMTATQYVAPLMAFNPNPGYSDNS 190
Db 61 QARVNLSDFFEPFYGHFLREITVATGCFYTGVEVHRLMTATQYIAPLMANFDPVSRRNS 120
QY 191 TVYFNGTVFVQWQDHVYLQGWEDKGSFTFQAAALHHDGRIVEFYAYKEIPMSYPEISSQH 250
Db 121 TVRYFDNGTALVQWQDHVYLQDNYNLGSFTFQATLLMDGRIIFYGYKEIPVLYTQISSNH 180
QY 251 PVKGTGLSDAFMLNPSFDVPSRRSIFFYHRIELDPKSVTMSAVEFTPLPTCLOHRSQ 310
Db 181 PVKVGUSDFAFVVVHRTQIQIPNVRRTIYFYHRLVQMSKITNISAVENTPLPTCLOFNRC 240
QY 311 DACMSDLTFNCMCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDDHDSASPD 370
Db 241 GPCVSSQIGFNCMCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDFQDDHDSASPD 300
QY 371 T--SFSYDGLTTSS--SSLFIDSLTETDTHKLNYPAGDGLQ--NNLSPKTKGTVPVHL 424
Db 301 TIGATTQPRVLTTRRAVTSQFPTSLPTEDDTKIALHLKDNAGSTDDSAEEKGKGLHA 360
QY 425 GTIVGTVLAVLVAAILLAGIYINGHPTSNALFFIERRPHHPAMKFRSHPDHSTYAEV 484
Db 361 GLIVGLLILVLAIVTAVILVTVYVYHHTTSAASIFFIERRPSRWPAKFRSGHGPAYAEV 420
QY 485 EPSGHEKEGMEAEQC 500
Db 421 EPVG-EKEGFIYSEQC 435

RESULT 13
US-10-125-923A-472
; Sequence 472, Application US/10125923A
; GENERAL INFORMATION:

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Pan, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC79
; CURRENT APPLICATION NUMBER: US/10/125,923A
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-125-923A-472
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Query Match 48.1%; Score 1294; DB 6; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.5e-104;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVVED-NHSYVVSRLYGPSPHSELWVDVAEANRSQVKIHTILSNTHR 130
DB 95 LLLDDGQDNNTQIEEDTDHNYIYSRIYGPSPDSASRDLVWVDQEKDKVKGILSNTHR 154
QY 131 QASRVVLSDFPFYGHPLRQITATGGFIFMGDVHRLMTATQYVAPLMANFPGYSDNS 190
DB 155 QAARVNLSDPFYGHFLREITVATGGFITYGEVVRHMLTATQYIAPLMANFDPVSRSNS 214
QY 191 TVVYFDNGTVFVQWVDHVLQGWEDKGSFTFQAALHHDGRIVFAYPEKIPMSVPEISSQH 250
DB 215 TVRYFDNGTALVQWVDHVLQDNVNLGSGFTFQATLLMDGRILFYKKEIPVLVTQISSTNH 274
QY 251 PVKTLGLSDAFMILNPSDPVPESSRRSFEYHRIELDFSKVTSMSAVEFTPLTCLQHRSC 310
DB 275 PVKGLSDAFVVRHRIQIPNVRRITVEYHVRVLMQSKITNISAVEMTPTLCTCLQNRK 334
QY 311 DACMSDLTFNGSWCHVLQRCSSGDFRYQEWMDYGCQAEGRCNCEQFQEDHDHSDASPD 370
DB 335 GPCVSSQIGFNGSWCSKLRQCSGDFRHRQDWDVSGCPPEESKEKWCENTEPVTSSRTTT 394
QY 371 T--SFSPYDGLTTS--SSLFIDSLTDDTKLNPYAGGDLQ--NNLSPKTKGTPVHL 424
DB 395 TVGATTTQTRVLTTRRAVTSQFTSLPTEDDTKTAHLKDKNGASTDSSAEKKGGLHA 454
QY 425 GTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFTIERRPHHPAMKFRSHDPHTYAEV 484
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DB 455 GLIIGILVILVATAILVTVYMYHPTSAASIFFIERPSRWPAKFRROSGHPAYAEV 514
QY 485 EPSGHEKEGFMDEAQC 500
DB 515 EPVG-EKEGFIVSEQ 529

RESULT 14
US-10-205-892-472
; Sequence 472, Application US/10205892
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Pan, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC517
; CURRENT APPLICATION NUMBER: US/10/205,892
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-892-472
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Query Match 48.1%; Score 1294; DB 6; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.5e-104;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;

QY 72 LAMDTLPDNRTRVVED-NHSYVVSRLYGPSPHSELWVDVAEANRSQVKIHTILSNTHR 130
DB 95 LLLDDGQDNNTQIEEDTDHNYIYSRIYGPSPDSASRDLVWVDQEKDKVKGILSNTHR 154
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DB 155 QAARVNLSDPFYGHFLREITVATGGFITYGEVVRHMLTATQYIAPLMANFDPVSRSNS 214
QY 191 TVVYFDNGTVFVQWVDHVLQGWEDKGSFTFQAALHHDGRIVFAYPEKIPMSVPEISSQH 250
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QY 251 PVKTLGLSDAFMILNPSDPVPESSRRSFEYHRIELDFSKVTSMSAVEFTPLTCLQHRSC 310
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QY 371 T--SFSPYDGLTTS---SSLFIDSILTETDTPKLNYPAGDGLQ--NNLSPKTKGTPVHL 424
Db 395 TVGATTTQFRLVLTTRRAVTSQFPTSLPTEDDTKIALHLKNGASTDDSAEKKGGTLHA 454
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RESULT 15

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US-10-174-575-472
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C35
; CURRENT APPLICATION NUMBER: US/10/174,575
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 472
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-575-472

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Query Match 48.1%; Score 1294; DB 6; Length 529;
Best Local Similarity 57.1%; Pred. No. 2.5e-104;
Matches 249; Conservative 73; Mismatches 106; Indels 8; Gaps 5;
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Db 395 TVGATTTQFRLVLTTRRAVTSQFPTSLPTEDDTKIALHLKNGASTDDSAEKKGGTLHA 454
QY 425 GTIVGIVLAVLLVAAILIAGIYINGHPTSNAAALFFIERRPHHPWPAKFRSHPDHSTYAEV 484
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QY 485 EPSGHEKEGFMEAEQC 500
Db 515 EPVG-EKEGFIVSEQ 529

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Search completed: April 22, 2003, 16:14:52

Job time : 39 secs

GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 15:16:56 ; Search time 146 Seconds
(without alignments)
2207.990 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 500
Sequence: 1 MRGELMLVLVLRARALS.....YAEVPSGHEKGFMEAEQC 500

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending Patents_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	500	100.0	500	1	PCT-US02-08253-230
3	500	100.0	500	1	PCT-US02-29964-314
4	500	100.0	500	23	US-09-918-715-230
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6	500	100.0	500	27	US-60-327-731-15

7	500	100.0	527	1	PCT-US02-29964-804	Sequence 804, App
8	500	100.0	527	1	PCT-US02-29964-805	Sequence 805, App
9	500	100.0	527	27	US-60-327-731-3	Sequence 3, Appli
10	500	100.0	1002	1	PCT-US01-24031-179	Sequence 179, App
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14	395	79.0	488	1	PCT-US02-29964-315	Sequence 315, App
15	395	79.0	488	27	US-60-327-731-10	Sequence 10, Appl
16	377	75.4	470	27	US-60-327-731-12	Sequence 12, Appl
17	342	68.4	502	1	PCT-US02-16639-5	Sequence 5, Appli
18	342	68.4	502	25	US-10-156-487A-5	Sequence 5, Appli
19	271	54.2	431	1	PCT-US00-35260-36	Sequence 36, Appl
20	271	54.2	431	23	US-09-912-935-36	Sequence 36, Appl
21	271	54.2	431	25	US-10-168-365-36	Sequence 36, Appl
22	229	45.8	240	25	US-10-104-047-3712	Sequence 3712, Ap
23	224	44.8	528	27	US-60-242-679-1283	Sequence 1283, Ap
24	130	26.0	146	1	PCT-US01-16450-2453	Sequence 2453, Ap
25	130	26.0	146	1	PCT-US01-16450A-2453	Sequence 2453, Ap
26	108	21.6	205	1	PCT-US01-01354-16462	Sequence 16462, A
27	108	21.6	205	21	US-09-764-905-16462	Sequence 16462, A
28	108	21.6	205	24	US-10-092-399-16462	Sequence 16462, A
29	93	18.6	138	21	US-09-758-472-5729	Sequence 5729, Ap
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31	93	18.6	180	21	US-09-758-439-1069	Sequence 1069, Ap
32	93	18.6	180	26	US-10-201-915-1069	Sequence 1069, Ap
33	68	13.6	108	13	US-08-943-863A-38	Sequence 38, Appl
34	68	13.6	108	13	US-08-943-863B-38	Sequence 38, Appl
35	68	13.6	108	17	US-09-398-829-30	Sequence 30, Appl
36	53	10.6	53	1	PCT-US01-00663-32853	Sequence 32853, A
37	53	10.6	53	22	US-09-864-761-43750	Sequence 43750, A
38	53	10.6	53	25	US-10-182-993-31848	Sequence 31848, A
39	53	10.6	53	26	US-10-203-134-32631	Sequence 32631, A
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42	53	10.6	53	26	US-10-203-137-32853	Sequence 32853, A
43	53	10.6	53	26	US-10-203-139-31726	Sequence 31726, A
44	35	7.0	306	1	PCT-US01-08631-39678	Sequence 39678, A
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46	35	7.0	500	1	PCT-US01-24031-297	Sequence 297, App
47	35	7.0	500	1	PCT-US02-08253-192	Sequence 192, App
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50	35	7.0	500	23	US-09-918-715-297	Sequence 297, App
51	35	7.0	500	25	US-10-156-487A-6	Sequence 6, Appli
52	35	7.0	500	25	US-10-156-487A-6	Sequence 7, Appli
53	18	3.6	18	27	US-60-327-731-7	Sequence 13, Appl
54	17	3.4	17	27	US-60-327-731-13	Sequence 13, Appl
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64	10	2.0	392	21	US-09-764-325A-25	Sequence 25, Appl
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71	10	2.0	425	25	US-10-168-365-35	Sequence 35, Appl
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75	10	2.0	449	1	PCT-US00-35260-34	Sequence 34, Appl
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572	10	2.0	529	26	US-10-205-511-472	Sequence 472, App	645	10	2.0	530	23	US-09-918-715-299	Sequence 299, App
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575	10	2.0	529	26	US-10-205-891-472	Sequence 472, App	648	9	1.8	719	27	US-60-242-679-1423	Sequence 1423, App
576	10	2.0	529	26	US-10-205-893-472	Sequence 472, App	649	8	1.6	105	27	US-60-192-739-2382	Sequence 2382, App
577	10	2.0	529	26	US-10-205-894-472	Sequence 472, App	650	8	1.6	143	27	US-60-194-243-1705	Sequence 1705, App
578	10	2.0	529	26	US-10-205-895-472	Sequence 472, App	651	8	1.6	143	21	US-09-758-472-9461	Sequence 9461, App
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586	10	2.0	529	26	US-10-205-903-472	Sequence 472, App	659	8	1.6	317	21	US-09-902-540-9859	Sequence 9859, App
587	10	2.0	529	26	US-10-205-904-472	Sequence 472, App	660	8	1.6	388	21	US-09-791-537-52224	Sequence 52224, A
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843	7	1.4	260	1	PCT-US99-22853B-154	Sequence 154, App	917	7	1.4	388	12	US-08-833-457-350	Sequence 350, App
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849	7	1.4	260	27	US-60-191-681-13331	Sequence 13331, A	923	7	1.4	388	24	US-10-072-851-11458	Sequence 11623, A
850	7	1.4	264	27	US-60-243-468-1059	Sequence 1059, Ap	924	7	1.4	388	24	US-10-072-851-11623	Sequence 25430, A
851	7	1.4	267	1	PCT-US01-08631-33597	Sequence 33597, A	925	7	1.4	394	21	US-09-417-507-25430	Sequence 89738, A
852	7	1.4	270	21	US-09-738-626-5968	Sequence 5968, Ap	926	7	1.4	394	21	US-09-791-537-89738	Sequence 15525, A
853	7	1.4	274	1	PCT-US00-26524B-5039	Sequence 5039, Ap	927	7	1.4	395	27	US-60-360-039-15525	Sequence 16272, A
854	7	1.4	274	1	PCT-US00-35017A-1332	Sequence 1332, Ap	928	7	1.4	395	27	US-60-360-039-16272	Sequence 24386, A
855	7	1.4	274	25	US-10-106-698-5049	Sequence 5049, Ap	929	7	1.4	399	18	US-09-417-507-24386	Sequence 4, Appl
856	7	1.4	275	16	US-09-252-991A-19583	Sequence 19583, A	930	7	1.4	401	11	US-08-728-747-4	Sequence 17445, A
857	7	1.4	291	16	US-09-270-767-33107	Sequence 33107, A	931	7	1.4	401	20	US-09-629-469A-17446	Sequence 1048, Ap
858	7	1.4	291	16	US-09-270-767-48324	Sequence 48324, A	932	7	1.4	401	27	US-60-389-987-1048	Sequence 1048, Ap
859	7	1.4	291	16	US-09-270-849B-189592	Sequence 189592, A	933	7	1.4	401	27	US-60-412-418-1048	Sequence 15896, A
860	7	1.4	293	1	PCT-US01-08656-7556	Sequence 7556, Ap	934	7	1.4	403	27	US-60-360-039-15896	Sequence 8600, Ap
861	7	1.4	299	1	PCT-US01-01332-1150	Sequence 1150, Ap	935	7	1.4	405	16	US-09-252-691-8600	Sequence 8600, Ap
862	7	1.4	299	1	PCT-US01-01348-388	Sequence 388, App	936	7	1.4	405	16	US-09-252-691C-8600	Sequence 9770, A
863	7	1.4	299	21	US-09-764-870-388	Sequence 388, App	937	7	1.4	406	21	US-09-791-537-97770	Sequence 48120, A
864	7	1.4	299	21	US-09-764-875-1150	Sequence 1150, Ap	938	7	1.4	406	21	US-09-219-999-48120	Sequence 30117, A
865	7	1.4	299	25	US-10-125-540-388	Sequence 388, App	939	7	1.4	407	26	US-60-324-109-30117	Sequence 33, Appl
866	7	1.4	303	17	US-09-303-5180-690	Sequence 690, App	940	7	1.4	407	27	US-09-252-991A-27845	Sequence 33, Appl
867	7	1.4	304	24	US-10-015-127-13054	Sequence 13054, A	941	7	1.4	409	1	PCT-US02-07215-33	Sequence 33, Appl
868	7	1.4	310	21	US-09-791-537-30560	Sequence 30560, A	942	7	1.4	409	24	US-10-094-944-33	Sequence 33, Appl
869	7	1.4	313	1	PCT-US00-05881-741	Sequence 741, App	943	7	1.4	411	27	US-60-212-664-590	Sequence 590, App
870	7	1.4	313	23	US-09-925-298-741	Sequence 741, App	944	7	1.4	411	15	US-09-134-000-6481	Sequence 6481, Ap
871	7	1.4	313	25	US-10-102-806-741	Sequence 741, App	945	7	1.4	413	15	US-09-708-427-51140	Sequence 51140, A
872	7	1.4	316	19	US-09-543-681A-4590	Sequence 4590, Ap	946	7	1.4	416	21	US-09-791-537-73311	Sequence 73311, A
873	7	1.4	319	18	US-09-417-507-40259	Sequence 40259, A	947	7	1.4	417	16	US-09-254-472-7	Sequence 6, Appl
874	7	1.4	326	1	PCT-US02-07355-76	Sequence 76, Appl	948	7	1.4	417	17	US-09-382-088-6	Sequence 6, Appl
875	7	1.4	326	1	PCT-US02-07355-78	Sequence 78, Appl	949	7	1.4	417	17	US-09-382-088A-6	Sequence 6, Appl
876	7	1.4	330	15	US-09-154-707-203	Sequence 203, App	950	7	1.4	417	21	US-09-708-427-69871	Sequence 69871, A
877	7	1.4	330	15	US-09-154-707A-203	Sequence 203, App	951	7	1.4	417	21	US-09-791-537-11207	Sequence 11207, A
878	7	1.4	330	16	US-09-270-767-44544	Sequence 44544, A	952	7	1.4	417	21	US-09-791-537-75456	Sequence 75456, A
879	7	1.4	330	23	US-09-966-262-203	Sequence 203, App	953	7	1.4	417	21	US-09-791-537-85854	Sequence 85854, A
880	7	1.4	330	23	US-09-983-966-203	Sequence 203, App	954	7	1.4	417	21	US-09-791-537-129593	Sequence 129593
881	7	1.4	330	23	US-09-984-245-203	Sequence 203, App	955	7	1.4	417	21	US-09-791-537-132269	Sequence 132269
882	7	1.4	330	24	US-10-059-395-203	Sequence 203, App	955	7	1.4	417	23	US-09-933-642-7	Sequence 7, Appl

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956 7 1.4 418 21 US-09-791-537-81081
957 7 1.4 419 1 PCT-US01-24031-230
958 7 1.4 419 23 US-09-925-300-1506
959 7 1.4 421 21 US-09-758-472-9174
960 7 1.4 421 26 US-10-235-926-9174
961 7 1.4 423 20 US-09-605-703B-322
962 7 1.4 423 20 US-09-605-703B-324
963 7 1.4 423 21 US-09-738-626-3570
964 7 1.4 425 16 US-09-252-991A-31834
965 7 1.4 430 21 US-09-791-537-52328
966 7 1.4 432 23 US-09-925-388-8
967 7 1.4 432 21 US-09-791-537-32390
968 7 1.4 438 19 US-09-543-681A-9247
969 7 1.4 441 16 US-09-252-991A-24012
970 7 1.4 441 21 US-09-708-427-13243
971 7 1.4 443 22 US-09-855-768-900
972 7 1.4 449 1 PCT-US01-18569-2617
973 7 1.4 449 21 US-09-708-427-69870
974 7 1.4 449 24 US-10-091-007-22
975 7 1.4 449 26 US-10-264-049-2617
976 7 1.4 452 21 US-09-791-537-36334
977 7 1.4 453 19 US-09-513-996A-37844
978 7 1.4 453 21 US-09-708-427-14143
979 7 1.4 454 20 US-09-614-150-6111
980 7 1.4 454 27 US-60-167-217-6229
981 7 1.4 454 27 US-60-173-464-4391
982 7 1.4 454 27 US-60-191-637-6129
983 7 1.4 454 27 US-60-191-681-4803
984 7 1.4 458 26 US-10-219-999-39097
985 7 1.4 458 27 US-60-312-544-8622
986 7 1.4 461 21 US-09-791-537-110219
987 7 1.4 463 1 PCT-US02-07355-74
988 7 1.4 463 1 PCT-US02-18354-10
989 7 1.4 463 19 US-09-573-655A-716
990 7 1.4 463 19 US-09-573-655B-716
991 7 1.4 463 20 US-09-629-469A-14290
992 7 1.4 463 27 US-60-214-601-4
993 7 1.4 467 1 PCT-US02-07355-80
994 7 1.4 469 27 US-60-150-584-1022
995 7 1.4 469 27 US-60-360-039-5491
996 7 1.4 470 1 PCT-US01-18569-2916
997 7 1.4 470 21 US-09-791-537-126519
998 7 1.4 470 26 US-10-264-049-2916
999 7 1.4 471 6 US-08-203-905A-2
1000 7 1.4 471 21 US-09-791-537-121995

Sequence 81081, A
Sequence 1506, Ap
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Sequence 9174, Ap
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Sequence 322, App
Sequence 324, App
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Sequence 31834, A
Sequence 52328, A
Sequence 8, Appli
Sequence 32390, A
Sequence 8247, Ap
Sequence 24012, A
Sequence 19243, A
Sequence 900, App
Sequence 2617, Ap
Sequence 69870, A
Sequence 22, Appl
Sequence 2617, Ap
Sequence 36334, A
Sequence 37844, A
Sequence 14143, A
Sequence 6111, Ap
Sequence 6229, Ap
Sequence 4991, Ap
Sequence 6129, Ap
Sequence 4803, Ap
Sequence 39097, A
Sequence 8622, Ap
Sequence 110219,
Sequence 74, Appl
Sequence 10, Appl
Sequence 716, App
Sequence 716, App
Sequence 14290, A
Sequence 4, Appli
Sequence 80, Appl
Sequence 1022, Ap
Sequence 5491, Ap
Sequence 2916, Ap
Sequence 126519,
Sequence 2916, Ap
Sequence 2, Appli
Sequence 121995,

ALIGNMENTS

RESULT 1
PCT-US01-24031-230
; Sequence 230, Application PC/TUS0124031
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: PCT/US01/24031
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 500; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US01-24031-230
Query Match 100.0%; Score 500; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAGKTGVRGWNRRARESPGHVSEPD 60
DB 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAGKTGVRGWNRRARESPGHVSEPD 60
QY 61 TQISQDLGGTTLAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDAEANSQVK 120
DB 61 TQISQDLGGTTLAMDTLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDAEANSQVK 120
QY 121 IHTILSNTHROASRVVLSFDPFYGHPRLQITATGGTFMGDVTHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVVLSFDPFYGHPRLQITATGGTFMGDVTHRMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKSGFTFQAALHHDGRIVFAYKEI 240
DB 181 NFNPYSDNSTVYVFDNGTVFVQWDHVLQGWEDKSGFTFQAALHHDGRIVFAYKEI 240
QY 241 SVPELSSSOHPVKTGLSDAFMLNPSDPVPSRRSIFEYHRIELDPKSVTMSAVEPT 300
DB 241 SVPELSSSOHPVKTGLSDAFMLNPSDPVPSRRSIFEYHRIELDPKSVTMSAVEPT 300
QY 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGDFDRYQEWMDYGCAGAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGDFDRYQEWMDYGCAGAEGRMCEDFQ 360
QY 361 DDHDSASPDTSFSDYDGLTSSSLFISLTTEDDTKLNPYAGGDLQNNLSPKTKGT 420
DB 361 DDHDSASPDTSFSDYDGLTSSSLFISLTTEDDTKLNPYAGGDLQNNLSPKTKGT 420
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DB 421 PVHLCTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
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DB 481 YAEVPSGHEKEGFMFAEQC 500

PCT-US02-08253-230
; Sequence 230, Application PC/TUS0208253
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: PCT/US02/08253
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; TYPE: PRT
; ORGANISM: Homo sapiens

PCT-US02-08253-230
Query Match 100.0%; Score 500; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRGELWLLVLVREARALSPQAGHDEGPGSGWAAGKTGVRGWNRRARESPGHVSEPD 60
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Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
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Db 61 TQSQDLGGGTAMDTLPDNRTRVVDNHNHYSYRSLYGPSEPHSRELWVDVAEANSQVK 120
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Db 181 NFNPYSDNSTVYFDNGTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEHRIELDPKSVTMSAVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEHRIELDPKSVTMSAVEFTP 300
Qy 301 LPTCLQHRSCDACMSSDLTFNCWSCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDEQ 360
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Qy 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

RESULT 3
PCT-US02-29964-314
; Sequence 314, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Duanrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03

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; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: dt_FL_genes Version 6.0
; SEQ ID NO 314
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-314

Query Match 100.0%; Score 500; DB 1; Length 500;
Best local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
Qy 61 TQSQDLGGGTAMDTLPDNRTRVVDNHNHYSYRSLYGPSEPHSRELWVDVAEANSQVK 120
Db 61 TQSQDLGGGTAMDTLPDNRTRVVDNHNHYSYRSLYGPSEPHSRELWVDVAEANSQVK 120
Qy 121 IHTILSNTHROASRVLSFDPFPGHPLRQITATGTFPMGDVIRHMLTATQYVAPLMA 180
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Qy 181 NFNPYSDNSTVYFDNGTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYFDNGTVFVQWHDVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEHRIELDPKSVTMSAVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEHRIELDPKSVTMSAVEFTP 300
Qy 301 LPTCLQHRSCDACMSSDLTFNCWSCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDEQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCWSCHVLRQCSGFDYRQEWMDYGCQAEGRMCEDEQ 360
Qy 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
Qy 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

RESULT 4
US-09-918-715-230
; Sequence 230, Application US/09918715
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11

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; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-230

Query Match      100.0%; Score 500; DB 23; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTPDNTRVVEDNHSYVSRLYGCPSEPHSRELWVDVAEANRSQVK 120
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTPDNTRVVEDNHSYVSRLYGCPSEPHSRELWVDVAEANRSQVK 120
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 301 LPTCLQHRSCDACMSDLTFNCNCHVLRQCSGDFDRYQEWMDYGCQAEGRMCEDFQ 360
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 301 LPTCLQHRSCDACMSDLTFNCNCHVLRQCSGDFDRYQEWMDYGCQAEGRMCEDFQ 360
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 361 DEHDHSDASPTSFSPYDGLTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGT 420
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 481 YAEVEPSGHEKEGFMEAEQC 500
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 481 YAEVEPSGHEKEGFMEAEQC 500
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60

RESULT 5
US-60-327-731-5
; Sequence 5, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
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US-60-327-731-5

Query Match      100.0%; Score 500; DB 27; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTPDNTRVVEDNHSYVSRLYGCPSEPHSRELWVDVAEANRSQVK 120
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTPDNTRVVEDNHSYVSRLYGCPSEPHSRELWVDVAEANRSQVK 120
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 121 IHTILSNTHROASRVVLSFDFPFYGHPLRQITATGGFIEMGDVIHRMLTATQYVAPLMA 180
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 181 NFNPYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 301 LPTCLQHRSCDACMSDLTFNCNCHVLRQCSGDFDRYQEWMDYGCQAEGRMCEDFQ 360
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 301 LPTCLQHRSCDACMSDLTFNCNCHVLRQCSGDFDRYQEWMDYGCQAEGRMCEDFQ 360
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 361 DEHDHSDASPTSFSPYDGLTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGT 420
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 361 DEHDHSDASPTSFSPYDGLTTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPKTKGT 420
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 481 YAEVEPSGHEKEGFMEAEQC 500
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60
QY 481 YAEVEPSGHEKEGFMEAEQC 500
Db 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPD 60

RESULT 6
US-60-327-731-15
; Sequence 15, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-15

Query Match      100.0%; Score 500; DB 27; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARESPGHVSEPD 60
DB 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
DB 61 TQSQDLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGTFIFMGDVIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGTFIFMGDVIHRMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTWYFDNGTVEVQWQDHVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 181 NFNPYSDNSTWYFDNGTVEVQWQDHVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKGTGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKVTSMGAVEFT 300
DB 241 SVPEISSQHPVKGTGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKVTSMGAVEFT 300
QY 301 LPTCLQHRSCDACSSDLTFCNCWCHVLRQCSGFDRIYQEWMDYGCQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACSSDLTFCNCWCHVLRQCSGFDRIYQEWMDYGCQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSITTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
DB 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSITTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVEPSGHEKEGFMFAEQC 500
DB 481 YAEVEPSGHEKEGFMFAEQC 500

RESULT 7
PCT-US02-29964-804
; Sequence 804, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Felyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Weng, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 809ACIP PCT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
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; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 992
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 804
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29964-804

Query Match 100.0%; Score 500; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARESPGHVSEPD 60
DB 28 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARESPGHVSEPD 87
QY 61 TQSQDLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
DB 88 TQSQDLGGGTAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 147
QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGTFIFMGDVIHRMLTATQYVAPLMA 180
DB 148 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGTFIFMGDVIHRMLTATQYVAPLMA 207
QY 181 NFNPYSDNSTWYFDNGTVEVQWQDHVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
DB 208 NFNPYSDNSTWYFDNGTVEVQWQDHVYLOGWEDKGSFTFOAALHHDGRIVFAYKEIPM 267
QY 241 SVPEISSQHPVKGTGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKVTSMGAVEFT 300
DB 268 SVPEISSQHPVKGTGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKVTSMGAVEFT 327
QY 301 LPTCLQHRSCDACSSDLTFCNCWCHVLRQCSGFDRIYQEWMDYGCQAEGRMCEDFQ 360
DB 328 LPTCLQHRSCDACSSDLTFCNCWCHVLRQCSGFDRIYQEWMDYGCQAEGRMCEDFQ 387
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSITTEDDTKLNYPYAGGDLQNNLSPKTKGT 420
DB 388 DEDHDSASPDTSFSPYDGLTSSSLFIDSITTEDDTKLNYPYAGGDLQNNLSPKTKGT 447
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
DB 448 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 507
QY 481 YAEVEPSGHEKEGFMFAEQC 500
DB 508 YAEVEPSGHEKEGFMFAEQC 527

RESULT 8
PCT-US02-29964-805
; Sequence 805, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Felyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
```

; APPLICANT: Goodrich, Ryle W.
 ; APPLICANT: Weng, Gezhi
 ; APPLICANT: Haley-Vicente, Dana
 ; APPLICANT: Drmanac, Radoje T
 ; TITLE OF INVENTION: Novel Nucleic Acids and
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 809ACIP PCT
 ; CURRENT APPLICATION NUMBER: PCT/US02/29964
 ; CURRENT FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: US 60/323,739
 ; PRIOR FILING DATE: 2001-09-19
 ; PRIOR APPLICATION NUMBER: US 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US 09/491,404
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: US 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: US 09/560,875
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/03800
 ; PRIOR FILING DATE: 2001-02-05
 ; PRIOR APPLICATION NUMBER: US 09/515,126
 ; PRIOR FILING DATE: 2000-02-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 992
 ; SOFTWARE: pt_Fl_genes Version 6.0
 ; SEQ ID NO 805
 ; LENGTH: 527
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PCT-US02-29964-805

Query Match 100.0%; Score 500; DB 1; Length 527;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSGWAAGTVRGNRRARESPGHVSEPD 60
 Db 28 MRGELWLLVLVLRRAALSPQAGHDEGPGSGWAAGTVRGNRRARESPGHVSEPD 87
 QY 61 TQLSQDLGGGT LAMDTLPDNRTRVVEDNHSYVSRLYGSPSEHRELWVDVAEANSQVK 120
 Db 88 TQLSQDLGGGT LAMDTLPDNRTRVVEDNHSYVSRLYGSPSEHRELWVDVAEANSQVK 147
 QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVVHRMLTATQYVAPLMA 180
 Db 148 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVVHRMLTATQYVAPLMA 207
 QY 181 NFNPGYSDNSTVYFDNGTVFVQWHDVYLGQWEDKGSFTFQALHHDGRIVFAYKEIPM 240
 Db 208 NFNPGYSDNSTVYFDNGTVFVQWHDVYLGQWEDKGSFTFQALHHDGRIVFAYKEIPM 267
 QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDP SKVTSMSAVEFTP 300
 Db 268 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDP SKVTSMSAVEFTP 327
 QY 301 LPTCLQHRSCDACMSSDLTFNCNCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 360
 Db 328 LPTCLQHRSCDACMSSDLTFNCNCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 387
 QY 361 DEHDASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420
 Db 388 DEHDASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 447
 QY 421 PVHLGTIVGIVLVAALLAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
 Db 448 PVHLGTIVGIVLVAALLAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 507

QY 481 YAEVPSGHEKEGFMEEQC 500
 Db 508 YAEVPSGHEKEGFMEEQC 527

RESULT 9

US-60-327-731-3
 ; Sequence 3, Application US/60327731
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Malabika
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Ren, Feiyan
 ; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
 ; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
 ; FILE REFERENCE: HYS-44
 ; CURRENT APPLICATION NUMBER: US/60/327,731
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: PCT/US00/35017
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 527
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-60-327-731-3

Query Match 100.0%; Score 500; DB 27; Length 527;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSGWAAGTVRGNRRARESPGHVSEPD 60
 Db 28 MRGELWLLVLVLRRAALSPQAGHDEGPGSGWAAGTVRGNRRARESPGHVSEPD 87
 QY 61 TQLSQDLGGGT LAMDTLPDNRTRVVEDNHSYVSRLYGSPSEHRELWVDVAEANSQVK 120
 Db 88 TQLSQDLGGGT LAMDTLPDNRTRVVEDNHSYVSRLYGSPSEHRELWVDVAEANSQVK 147
 QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVVHRMLTATQYVAPLMA 180
 Db 148 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVVHRMLTATQYVAPLMA 207
 QY 181 NFNPGYSDNSTVYFDNGTVFVQWHDVYLGQWEDKGSFTFQALHHDGRIVFAYKEIPM 240
 Db 208 NFNPGYSDNSTVYFDNGTVFVQWHDVYLGQWEDKGSFTFQALHHDGRIVFAYKEIPM 267
 QY 241 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDP SKVTSMSAVEFTP 300
 Db 268 SVPEISSQHVPKVTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDP SKVTSMSAVEFTP 327
 QY 301 LPTCLQHRSCDACMSSDLTFNCNCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 360
 Db 328 LPTCLQHRSCDACMSSDLTFNCNCHVLRQCSGFDRIYRQWMDYGCQAEGRMCEDFQ 387
 QY 361 DEHDASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420
 Db 388 DEHDASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 447
 QY 421 PVHLGTIVGIVLVAALLAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
 Db 448 PVHLGTIVGIVLVAALLAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 507
 QY 481 YAEVPSGHEKEGFMEEQC 500
 Db 508 YAEVPSGHEKEGFMEEQC 527

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RESULT 10
PCT-US01-24031-179
; Sequence 179, Application PC/TUS0124031
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: PCT/US01/24031
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-24031-179

Query Match      100.0%; Score 500; DB 1; Length 1002;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPR 60
Db 503 MRGELWLLVLRRAARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPR 562

QY 61 TQLSQDLGGGTLMADTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
Db 563 TQLSQDLGGGTLMADTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 622

QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVTHRMULTATQYVAPLMA 180
Db 623 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVTHRMULTATQYVAPLMA 682

QY 181 NFNPGYSDNSTVVFYDNGTVFVQWDHVLQGWEDKSGFTFOAALHHDGRIVFAYKEIPM 240
Db 683 NFNPGYSDNSTVVFYDNGTVFVQWDHVLQGWEDKSGFTFOAALHHDGRIVFAYKEIPM 742

QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRSIFEXHRIELDSPKVTSMASVEFTP 300
Db 743 SVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRSIFEXHRIELDSPKVTSMASVEFTP 802

QY 301 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSGFDTRYQEWMDYGCQAEGRMCEDFQ 360
Db 803 LPTCLQHRSCDACMSDLTFNCSCWCHVLRQCSGFDTRYQEWMDYGCQAEGRMCEDFQ 862

QY 361 DEDHDSASPDTSFSDYDGLTTSSSLFIDSLTDDTKLNPYAGGDLQNNLSPKTKGT 420
Db 863 DEDHDSASPDTSFSDYDGLTTSSSLFIDSLTDDTKLNPYAGGDLQNNLSPKTKGT 922

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERPHHPAMKFRSHPDHST 480
Db 923 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERPHHPAMKFRSHPDHST 982

QY 481 YAEVPSGHEKEGFMEEAQC 500
Db 983 YAEVPSGHEKEGFMEEAQC 1002

RESULT 11
PCT-US02-08253-179
; Sequence 179, Application PC/TUS0208253
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
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; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-179

Query Match 100.0%; Score 500; DB 23; Length 1002;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGELWLVLVLRRAARALSPQAGHDEGPGSGAAAGTVRGNRRARESPGHVSEPD 60
DB 503 MRGELWLVLVLRRAARALSPQAGHDEGPGSGAAAGTVRGNRRARESPGHVSEPD 562
QY 61 TQSLDGLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 120
DB 563 TQSLDGLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVK 622
QY 121 IHTILSNTHRQASRVLSFDFPFYCHPLRQITTIATGGFIFMGDVIHRLMTATQYVAPLMA 180
DB 623 IHTILSNTHRQASRVLSFDFPFYCHPLRQITTIATGGFIFMGDVIHRLMTATQYVAPLMA 682
QY 181 NFNGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
DB 683 NFNGYSDNSTVYFDNGTVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 742
QY 241 SVPEISSQHPVKTKGLSDAPMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
DB 743 SVPEISSQHPVKTKGLSDAPMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 802
QY 301 LPTCLOHRSQDACSMDLTFNCSCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 360
DB 803 LPTCLOHRSQDACSMDLTFNCSCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFQ 862
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTETDTPKLNYPAGGDLQNNLSPTKGT 420
DB 863 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTETDTPKLNYPAGGDLQNNLSPTKGT 922
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHST 480
DB 923 PVHLGTIVGIVLAVLLVAAILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHST 982
QY 481 YAEVPSGHEKEGFMEEQC 500
DB 983 YAEVPSGHEKEGFMEEQC 1002

RESULT 13
US-60-327-731-8
; Sequence 8, Application US/60327731
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44
; CURRENT APPLICATION NUMBER: US/60/327,731
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 482

; TYPE: PRT
; ORGANISM: homo sapiens
US-60-327-731-8

Query Match 96.4%; Score 482; DB 27; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DNRTRVEDNHSYVSRLYGPPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVLS 120
QY 139 FDPFFYCHPLRQITTIATGGFIFMGDVIHRLMTATQYVAPLMAFNPNGYSDNSTVYFDNG 198
DB 121 FDPFFYCHPLRQITTIATGGFIFMGDVIHRLMTATQYVAPLMAFNPNGYSDNSTVYFDNG 180
QY 199 TVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKGLSD 258
DB 181 TVFVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKGLSD 240
QY 259 AFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTPCTCLOHRSQDACSMDL 318
DB 241 AFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTPCTCLOHRSQDACSMDL 300
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DB 301 TFNCSCWCHVLRQCSGFDRIYQWMDYGCQAEGRMCEDFODEHDSASPDTSFSPYDG 360
QY 379 DLTTSSSLFIDSLTETDTPKLNYPAGGDLQNNLSPTKGTTPVHLGTIVGIVLAVLLVA 438
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DB 421 AILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEGFMEE 480
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DB 481 QC 482

RESULT 14
PCT-US02-29964-315
; Sequence 315, Application PC/TUS0229964
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Dunrui
; APPLICANT: Ghosh, Malabika
; APPLICANT: Asundi, Vinod
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle W.
; APPLICANT: Wang, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 809ACIP ECT
; CURRENT APPLICATION NUMBER: PCT/US02/29964
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,739
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21

;; PRIOR APPLICATION NUMBER: US 09/552,317
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: PCT/US00/35017
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: US 09/491,404
;; PRIOR FILING DATE: 2000-01-25
;; PRIOR APPLICATION NUMBER: PCT/US01/02623
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: US 09/496,914
;; PRIOR FILING DATE: 2000-02-03
;; PRIOR APPLICATION NUMBER: US 09/560,875
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: PCT/US01/03800
;; PRIOR FILING DATE: 2001-02-05
;; PRIOR APPLICATION NUMBER: US 09/515,126
;; PRIOR FILING DATE: 2000-02-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 992
;; SOFTWARE: pt_FL_genes Version 6.0
;; SEQ ID NO 315
;; LENGTH: 488
;; TYPE: PRT
;; ORGANISM: Homo sapiens
PCT-US02-29964-315

Query Match 79.0%; Score 395; DB 1; Length 488;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 SVPEISSSQHPVKTGLSDAFMILNPSDPVPESSRRSIFFEYHRIELDPKSVTMSAVEFTP 300

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DB 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTE 395

RESULT 15
US-60-327-731-10
;; Sequence 10, Application US/60327731
;; GENERAL INFORMATION:
;; APPLICANT: Ghosh, Malabika
;; APPLICANT: Tang, Y. Tom
;; APPLICANT: Ren, Feiyan
;; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
;; FILE REFERENCE: HYS-44
;; CURRENT APPLICATION NUMBER: US/60/327,731
;; PRIOR FILING DATE: 2001-10-05
;; PRIOR APPLICATION NUMBER: PCT/US00/35017
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 09/552,317

;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: Patent in version 3.1
;; SEQ ID NO 10
;; LENGTH: 488
;; TYPE: PRT
;; ORGANISM: homo sapiens
US-60-327-731-10

Query Match 79.0%; Score 395; DB 27; Length 488;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TQLSODLGGGTLMADTLPDNRTRVVDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
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QY 121 IHTILSNTHROASRVVLSDFPFYGHPLRQITATGGFIFMGDVTHRMILTATQYVAPLMA 180
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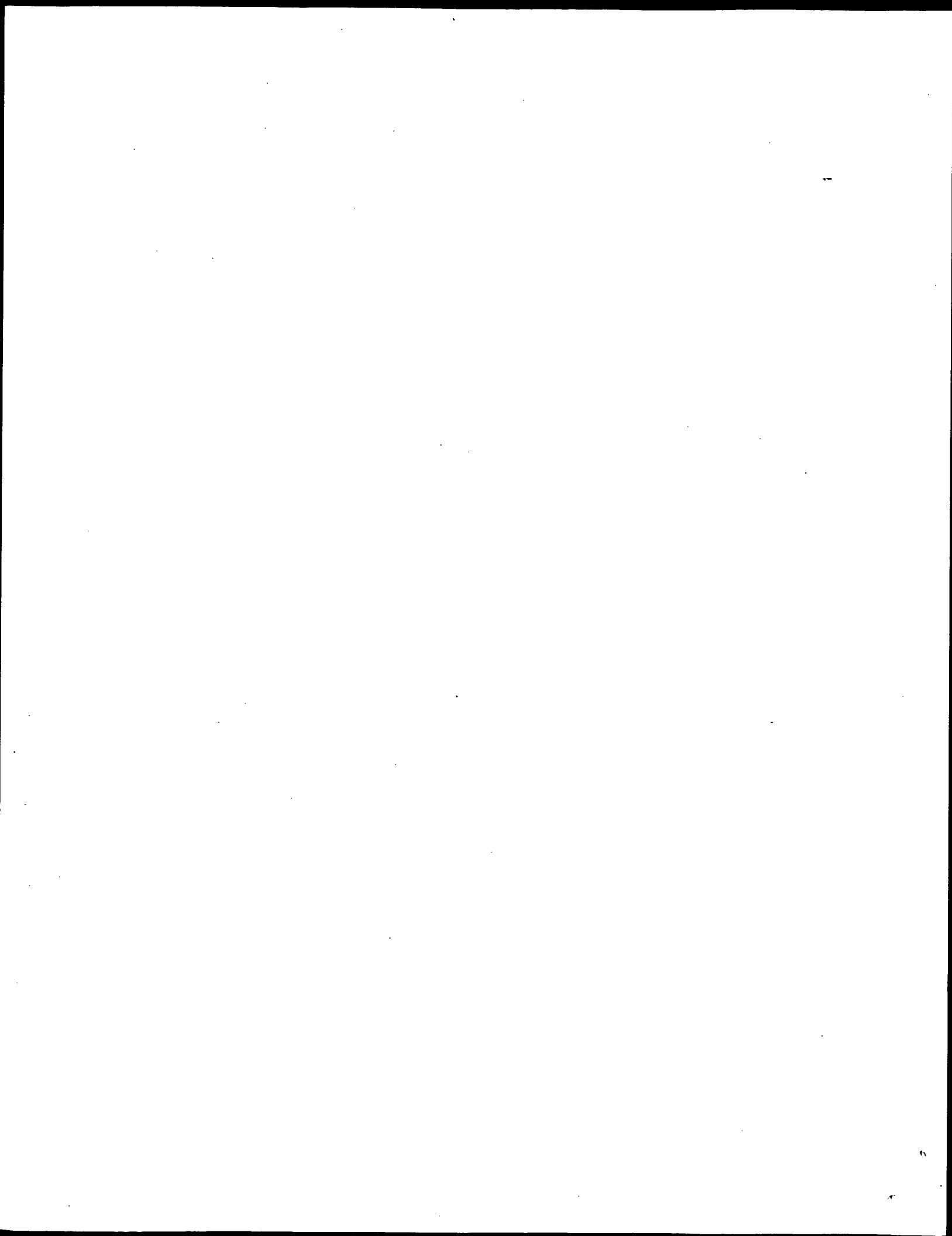
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DB 301 LPTCLQHRSCDACMSDLTFNCNCHVLQRCSSGFDYRQEWMDYGCQAQAEGRMCEDFQ 360

QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTE 395
DB 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTE 395

Search completed: April 22, 2003, 16:23:00
Job time : 179 secs



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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:17:11 ; Search time 79 Seconds
(without alignments)
998.686 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 500

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	500	100.0	527	6	US-10-266-252-3
6	482	96.4	482	6	US-10-266-252-8
7	427	85.4	427	7	US-60-453-135-13630
8	427	85.4	427	7	US-60-453-050-13630
9	395	79.0	488	6	US-10-266-252-10
10	377	75.4	470	6	US-10-266-252-12
11	371	74.2	400	6	US-10-218-140-5790
12	130	26.0	146	6	US-10-264-237-2453
13	130	26.0	146	6	US-10-266-252-7
14	17	3.4	17	6	US-10-266-252-13
15	10	2.0	290	6	US-10-218-140-526
16	10	2.0	379	7	US-60-452-680-20245
17	10	2.0	435	6	US-10-266-252-14
18	10	2.0	529	6	US-10-125-923A-472
19	10	2.0	529	6	US-10-205-892-472
20	10	2.0	529	6	US-10-174-575-472
21	10	2.0	529	6	US-10-174-575A-472
22	10	2.0	529	6	US-10-187-755-472
23	10	2.0	529	6	US-10-187-749-472
24	10	2.0	529	6	US-10-199-672-472
25	10	2.0	529	6	US-10-194-486-472
26	10	2.0	530	1	PCT-US02-34451-12

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29	8	1.6	505	6	US-10-156-761-14310	Sequence 14310, A
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31	8	1.6	1004	1	PCT-US02-07283-58	Sequence 58, Appl
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36	7	1.4	8	5	US-09-641-528-28138	Sequence 28138, A
37	7	1.4	8	5	US-09-641-528-45901	Sequence 45901, A
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62	7	1.4	10	5	US-09-641-528-6626	Sequence 6626, Ap
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103	7	1.4	15	US-09-641-528A-47648	Sequence 47648, A	176	7	1.4	346	6	US-10-366-683-14945	Sequence 14945, A
104	7	1.4	15	US-09-641-528A-47650	Sequence 47650, A	177	7	1.4	348	6	US-10-366-683-19684	Sequence 19684, A
105	7	1.4	15	US-09-641-528A-47651	Sequence 47651, A	178	7	1.4	347	6	US-10-366-683-24649	Sequence 24649, A
106	7	1.4	15	US-09-641-528A-47651	Sequence 47651, A	179	7	1.4	377	6	US-10-366-683-24649	Sequence 24649, A
107	7	1.4	15	US-09-641-528A-47621	Sequence 47621, A	180	7	1.4	388	6	US-10-282-122A-59031	Sequence 59031, A
108	7	1.4	15	US-09-641-528A-47633	Sequence 47633, A	181	7	1.4	388	6	US-10-335-977-5797	Sequence 5797, Ap
109	7	1.4	15	US-09-641-528A-47648	Sequence 47648, A	182	7	1.4	395	6	US-10-369-493-15525	Sequence 15525, A
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111	7	1.4	68	PCT-US02-32727-6277	Sequence 6277, Ap	184	7	1.4	403	5	US-09-949-016-8892	Sequence 8891, Ap
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115	7	1.4	97	US-10-188-246-24	Sequence 24, Appl	188	7	1.4	411	7	US-60-453-050-9757	Sequence 9757, Ap
116	7	1.4	99	PCT-US02-21360-22	Sequence 54, Appl	189	7	1.4	411	7	US-60-453-050-9758	Sequence 9758, Ap
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118	7	1.4	101	US-10-188-246-22	Sequence 22, Appl	191	7	1.4	413	5	US-09-134-000C-6481	Sequence 6481, Ap
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124	7	1.4	114	US-09-978-825-25797	Sequence 25797, A	197	7	1.4	418	1	PCT-US02-37431-187	Sequence 187, App
125	7	1.4	114	US-10-188-246-20	Sequence 20, Appl	198	7	1.4	418	1	US-09-949-016-6044	Sequence 6044, Ap
126	7	1.4	114	US-10-188-246-20	Sequence 20, Appl	199	7	1.4	420	1	PCT-US02-32727-24800	Sequence 187, App
127	7	1.4	124	US-10-366-683-21089	Sequence 21089, A	200	7	1.4	420	5	US-09-978-825-24800	Sequence 24800, A
128	7	1.4	129	PCT-US02-32727-7531	Sequence 7531, Ap	201	7	1.4	420	5	US-10-057-498-24800	Sequence 24800, A
129	7	1.4	129	US-09-978-825-7531	Sequence 7531, Ap	202	7	1.4	422	5	US-09-949-016-9517	Sequence 9517, Ap
130	7	1.4	129	US-10-057-498-7531	Sequence 7531, Ap	203	7	1.4	422	5	US-09-949-016-9518	Sequence 9518, Ap
131	7	1.4	137	US-09-675-784A-7983	Sequence 7983, Ap	204	7	1.4	425	6	US-10-366-683-31834	Sequence 31834, A
132	7	1.4	144	US-10-282-122A-49872	Sequence 49872, A	205	7	1.4	439	7	US-60-443-566-4365	Sequence 4365, Ap
133	7	1.4	144	US-10-156-761-10524	Sequence 10524, A	206	7	1.4	439	7	US-60-453-444-8375	Sequence 8375, Ap
134	7	1.4	191	US-09-675-784A-8693	Sequence 8693, Ap	207	7	1.4	441	6	US-10-366-683-24012	Sequence 24012, A
135	7	1.4	194	US-09-828-455-27	Sequence 27, Appl	208	7	1.4	449	5	US-09-769-736-135	Sequence 135, App
136	7	1.4	194	US-09-828-455-27	Sequence 27, Appl	209	7	1.4	449	5	US-09-949-016-9515	Sequence 9515, Ap
137	7	1.4	197	US-10-094-749-2714	Sequence 2714, Ap	210	7	1.4	449	5	US-09-949-016-9516	Sequence 9516, Ap
138	7	1.4	204	US-09-949-002-457	Sequence 457, App	211	7	1.4	463	6	US-10-094-886A-74	Sequence 74, Appl
139	7	1.4	204	US-10-156-761-9250	Sequence 9250, Ap	212	7	1.4	463	6	US-10-312-354-8	Sequence 8, Appl
140	7	1.4	213	US-10-156-761-9250	Sequence 9250, Ap	213	7	1.4	463	6	US-10-094-886A-74	Sequence 74, Appl
141	7	1.4	215	US-10-156-761-12773	Sequence 12773, A	214	7	1.4	463	7	US-60-443-566-4364	Sequence 4364, Ap
142	7	1.4	221	PCT-US02-35136-9	Sequence 9, Appl	215	7	1.4	463	7	US-60-453-444-8374	Sequence 8374, Ap
143	7	1.4	227	US-10-366-683-25207	Sequence 25207, A	216	7	1.4	463	7	US-10-094-886A-80	Sequence 80, Appl
144	7	1.4	229	PCT-US02-32727-18027	Sequence 18027, A	217	7	1.4	466	6	US-10-369-493-5491	Sequence 5491, Appl
145	7	1.4	229	US-09-978-825-18027	Sequence 18027, A	218	7	1.4	466	6	US-10-369-493-5491	Sequence 5491, Appl
146	7	1.4	229	US-10-057-498-18027	Sequence 18027, A	219	7	1.4	471	5	US-09-949-016-6774	Sequence 6774, Ap
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148	7	1.4	233	US-10-335-977-5795	Sequence 5795, Ap	221	7	1.4	483	5	US-09-949-016-11046	Sequence 11046, A
149	7	1.4	233	US-10-335-977-5795	Sequence 5795, Ap	222	7	1.4	483	6	US-10-366-683-27160	Sequence 27160, A
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151	7	1.4	275	US-10-366-683-19383	Sequence 19383, A	224	7	1.4	498	6	US-10-369-493-23601	Sequence 23601, A
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153	7	1.4	280	US-60-452-680-18564	Sequence 18564, A	226	7	1.4	500	7	US-60-443-566-4425	Sequence 4425, Ap
154	7	1.4	280	US-60-453-135-11148	Sequence 11148, A	227	7	1.4	500	7	US-60-452-680-18563	Sequence 18563, A
155	7	1.4	280	US-60-453-050-11148	Sequence 11148, A	228	7	1.4	500	7	US-60-453-135-11147	Sequence 11147, A
156	7	1.4	280	US-60-453-050-11148	Sequence 11148, A	229	7	1.4	500	7	US-60-453-050-11147	Sequence 11147, A
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158	7	1.4	282	PCT-US02-32727-23151	Sequence 23151, A	231	7	1.4	520	6	US-10-223-076-3	Sequence 3, Appl
159	7	1.4	282	US-09-978-825-23151	Sequence 23151, A	232	7	1.4	520	6	US-10-361-942-514	Sequence 514, App
160	7	1.4	282	US-09-978-825-23151	Sequence 23151, A	233	7	1.4	529	7	US-60-452-680-12463	Sequence 12463, A
161	7	1.4	282	US-10-057-498-23151	Sequence 23151, A	234	7	1.4	535	6	US-10-224-209-2	Sequence 2, Appl
162	7	1.4	315	US-09-724-676A-78605	Sequence 78605, A	235	7	1.4	545	6	US-10-369-493-7880	Sequence 7880, Ap
163	7	1.4	315	US-09-724-676A-78605	Sequence 78605, A	236	7	1.4	545	6	US-10-366-683-23813	Sequence 23813, A
164	7	1.4	315	US-09-724-676A-78605	Sequence 78605, A	237	7	1.4	554	6	US-10-282-122A-72403	Sequence 72403, A
165	7	1.4	315	US-09-724-676A-78605	Sequence 78605, A	238	7	1.4	561	6	US-10-366-683-22327	Sequence 22327, A
166	7	1.4	321	US-10-282-122A-66162	Sequence 66162, A	239	7	1.4	596	6	US-10-366-683-20097	Sequence 20097, A
167	7	1.4	326	US-10-094-886-76	Sequence 76, Appl	240	7	1.4	608	6	US-10-366-683-18239	Sequence 18239, A
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169	7	1.4	326	US-10-094-886A-76	Sequence 76, Appl	242	7	1.4	613	6	PCT-US02-37777-38	Sequence 38, Appl
170	7	1.4	326	US-10-094-886A-76	Sequence 76, Appl	243	7	1.4	623	5		
171	7	1.4	327	US-10-282-122A-64027	Sequence 64027, A	244	7	1.4	631	1		
172	7	1.4	327			245	7	1.4	631	1		

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248	7	1.4	654	6	US-10-366-683-31667	Sequence 31667, A	321	7	1.4	1184	6	US-10-127-845A-412	Sequence 412, App
249	7	1.4	660	5	US-09-724-676-78601	Sequence 78601, A	322	7	1.4	1184	6	US-10-127-846A-412	Sequence 412, App
250	7	1.4	660	5	US-09-724-676-78601	Sequence 78604, A	323	7	1.4	1184	6	US-10-127-847A-412	Sequence 412, App
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252	7	1.4	660	5	US-09-724-676-78601	Sequence 78604, A	325	7	1.4	1184	6	US-10-127-851A-412	Sequence 412, App
253	7	1.4	660	6	US-10-263-929-110	Sequence 110, App	326	7	1.4	1184	6	US-10-127-852A-412	Sequence 412, App
254	7	1.4	684	6	US-10-156-761-12753	Sequence 12753, A	327	7	1.4	1184	6	US-10-127-900A-412	Sequence 412, App
255	7	1.4	675	6	US-10-366-683-23185	Sequence 23185, A	328	7	1.4	1184	6	US-10-128-687A-412	Sequence 412, App
256	7	1.4	686	7	US-60-452-680-22413	Sequence 22413, A	329	7	1.4	1184	6	US-10-128-688A-412	Sequence 412, App
257	7	1.4	686	7	US-60-452-680-22413	Sequence 13882, A	330	7	1.4	1184	6	US-10-128-692A-412	Sequence 412, App
258	7	1.4	686	7	US-60-453-135-13882	Sequence 13882, A	331	7	1.4	1184	6	US-10-128-692A-412	Sequence 412, App
259	7	1.4	701	6	US-60-446-775-338	Sequence 338, App	332	7	1.4	1184	6	US-10-131-816A-412	Sequence 412, App
260	7	1.4	709	6	US-10-161-493-76	Sequence 76, Appl	333	7	1.4	1184	6	US-10-131-817A-412	Sequence 412, App
261	7	1.4	713	6	US-10-156-761-11362	Sequence 11362, A	334	7	1.4	1184	6	US-10-131-818A-412	Sequence 412, App
262	7	1.4	767	6	US-10-366-683-28262	Sequence 28262, A	335	7	1.4	1184	6	US-10-131-835A-412	Sequence 412, App
263	7	1.4	794	1	PCT-US02-28859-76	Sequence 76, Appl	336	7	1.4	1184	6	US-10-127-826A-412	Sequence 412, App
264	7	1.4	794	6	US-10-241-220-76	Sequence 76, Appl	337	7	1.4	1184	6	US-10-127-826A-412	Sequence 412, App
265	7	1.4	885	6	US-10-282-122A-43753	Sequence 43753, A	338	7	1.4	1184	6	US-10-127-828A-412	Sequence 412, App
266	7	1.4	1019	6	US-10-094-749-2609	Sequence 2609, App	339	7	1.4	1184	6	US-10-127-833A-412	Sequence 412, App
267	7	1.4	1065	6	US-10-282-122A-64932	Sequence 64932, A	340	7	1.4	1184	6	US-10-127-833A-412	Sequence 412, App
268	7	1.4	1093	6	US-10-369-493-10885	Sequence 10885, A	341	7	1.4	1184	6	US-10-131-825A-412	Sequence 412, App
269	7	1.4	1120	6	US-10-369-493-1495	Sequence 1495, App	342	7	1.4	1184	6	US-10-127-828A-412	Sequence 412, App
270	7	1.4	1144	7	US-60-452-680-22415	Sequence 22415, A	343	7	1.4	1184	6	US-10-131-815A-412	Sequence 412, App
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273	7	1.4	1184	5	US-09-989-733-124	Sequence 124, App	346	7	1.4	1184	6	US-10-131-828A-412	Sequence 412, App
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279	7	1.4	1184	6	US-10-131-826A-412	Sequence 412, App	352	7	1.4	1245	7	US-60-453-050-7845	Sequence 7845, App
280	7	1.4	1184	6	US-10-131-829A-412	Sequence 412, App	353	7	1.4	1250	7	US-60-449-155-64	Sequence 64, Appl
281	7	1.4	1184	6	US-10-125-926A-412	Sequence 412, App	354	7	1.4	1269	6	US-10-282-122A-62237	Sequence 62237, A
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285	7	1.4	1184	6	US-10-127-837A-412	Sequence 412, App	358	7	1.4	1330	7	US-60-453-135-13883	Sequence 13883, A
286	7	1.4	1184	6	US-10-127-842A-412	Sequence 412, App	359	7	1.4	1330	7	US-60-453-050-13883	Sequence 13883, A
287	7	1.4	1184	6	US-10-127-850A-412	Sequence 412, App	360	6	1.2	7	6	US-10-293-580-31	Sequence 31, Appl
288	7	1.4	1184	6	US-10-127-901A-412	Sequence 412, App	361	6	1.2	8	5	US-09-641-528-6037	Sequence 6037, App
289	7	1.4	1184	6	US-10-128-689A-412	Sequence 412, App	362	6	1.2	8	5	US-09-641-528-6588	Sequence 6588, App
290	7	1.4	1184	6	US-10-131-830A-412	Sequence 412, App	363	6	1.2	8	5	US-09-641-528-6624	Sequence 6624, App
291	7	1.4	1184	6	US-10-131-833A-412	Sequence 412, App	364	6	1.2	8	5	US-09-641-528-14449	Sequence 14449, A
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293	7	1.4	1184	6	US-10-125-930A-412	Sequence 412, App	366	6	1.2	8	5	US-09-641-528-22452	Sequence 22452, A
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295	7	1.4	1184	6	US-10-127-838B-412	Sequence 412, App	368	6	1.2	8	5	US-09-641-528-28094	Sequence 28094, A
296	7	1.4	1184	6	US-10-127-843A-412	Sequence 412, App	369	6	1.2	8	5	US-09-641-528A-6037	Sequence 6037, App
297	7	1.4	1184	6	US-10-127-849A-412	Sequence 412, App	370	6	1.2	8	5	US-09-641-528A-6588	Sequence 6588, App
298	7	1.4	1184	6	US-10-128-684A-412	Sequence 412, App	371	6	1.2	8	5	US-09-641-528A-6624	Sequence 6624, App
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302	7	1.4	1184	6	US-10-128-693A-412	Sequence 412, App	375	6	1.2	8	5	US-09-641-528A-22747	Sequence 22747, A
303	7	1.4	1184	6	US-10-131-821A-412	Sequence 412, App	376	6	1.2	8	5	US-09-641-528A-28094	Sequence 28094, A
304	7	1.4	1184	6	US-10-131-836A-412	Sequence 412, App	377	6	1.2	9	5	US-09-189-702A-117	Sequence 117, App
305	7	1.4	1184	6	US-10-137-872A-412	Sequence 412, App	378	6	1.2	9	5	US-09-641-528-1025	Sequence 1025, App
306	7	1.4	1184	6	US-10-137-873A-412	Sequence 412, App	379	6	1.2	9	5	US-09-641-528-1133	Sequence 1133, App
307	7	1.4	1184	6	US-10-125-921A-412	Sequence 412, App	380	6	1.2	9	5	US-09-641-528-6044	Sequence 6044, App
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314	7	1.4	1184	6	US-10-127-832A-412	Sequence 412, App	387	6	1.2	9	5	US-09-641-528-49748	Sequence 49748, A
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316	7	1.4	1184	6	US-10-127-836A-412	Sequence 412, App	389	6	1.2	9	5	US-09-641-528A-1153	Sequence 1153, App
317	7	1.4	1184	6	US-10-127-839A-412	Sequence 412, App	390	6	1.2	9	5	US-09-641-528A-6044	Sequence 6044, App
318	7	1.4	1184	6	US-10-127-840A-412	Sequence 412, App	391	6	1.2	9	5	US-09-641-528A-14450	Sequence 14450, A

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394	6	1.2	9	5	US-09-641-528A-22455	Sequence 22455, A	467	6	1.2	52	6	US-10-057-498-14560	Sequence 14560, A
395	6	1.2	9	5	US-09-641-528A-28095	Sequence 28095, A	468	6	1.2	52	6	US-10-057-498-20815	Sequence 20815, A
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398	6	1.2	10	5	US-09-641-528A-49748	Sequence 49748, A	471	6	1.2	53	5	US-09-864-408A-1036	Sequence 1036, Ap
399	6	1.2	10	5	US-09-189-702A-152	Sequence 152, App	472	6	1.2	53	5	US-09-864-408A-8076	Sequence 8076, Ap
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401	6	1.2	10	5	US-09-641-528-6589	Sequence 6589, Ap	474	6	1.2	53	6	US-10-218-140-1142	Sequence 1142, Ap
402	6	1.2	10	5	US-09-641-528-6612	Sequence 6612, Ap	475	6	1.2	54	1	PCT-US02-32727-21407	Sequence 21407, A
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405	6	1.2	10	5	US-09-641-528-28096	Sequence 28096, A	478	6	1.2	55	1	PCT-US02-32727-10194	Sequence 10194, A
406	6	1.2	10	5	US-09-641-528-35774	Sequence 35774, A	479	6	1.2	55	5	US-09-978-825-10194	Sequence 10194, A
407	6	1.2	10	5	US-09-641-528A-6216	Sequence 6216, Ap	480	6	1.2	55	6	US-10-057-498-10194	Sequence 10194, A
408	6	1.2	10	5	US-09-641-528A-6589	Sequence 6589, Ap	481	6	1.2	56	5	US-09-724-676-91592	Sequence 91592, A
409	6	1.2	10	5	US-09-641-528A-6612	Sequence 6612, Ap	482	6	1.2	56	5	US-09-724-676A-91592	Sequence 91592, A
410	6	1.2	10	5	US-09-641-528A-22571	Sequence 22571, A	483	6	1.2	56	6	US-10-282-122A-57361	Sequence 57361, A
411	6	1.2	10	5	US-09-641-528A-22745	Sequence 22745, A	484	6	1.2	57	5	US-09-864-408A-6222	Sequence 6222, Ap
412	6	1.2	10	5	US-09-641-528A-28096	Sequence 28096, A	485	6	1.2	58	6	US-10-315-023-15	Sequence 15, Appl
413	6	1.2	11	5	US-09-641-528A-35774	Sequence 35774, A	486	6	1.2	59	1	PCT-US02-32727-19633	Sequence 19633, A
414	6	1.2	11	5	US-09-641-528-1154	Sequence 1154, Ap	487	6	1.2	59	5	US-09-978-825-19633	Sequence 19633, A
415	6	1.2	11	5	US-09-641-528-6038	Sequence 6038, Ap	488	6	1.2	59	6	US-10-057-498-19633	Sequence 19633, A
416	6	1.2	11	5	US-09-641-528-6103	Sequence 6103, Ap	489	6	1.2	59	6	US-10-243-475-93	Sequence 93, Appl
417	6	1.2	11	5	US-09-641-528-14451	Sequence 14451, A	490	6	1.2	60	1	PCT-US02-32727-3865	Sequence 3865, Ap
418	6	1.2	11	5	US-09-641-528-14861	Sequence 14861, A	491	6	1.2	60	5	US-09-513-999C-6713	Sequence 6713, Ap
419	6	1.2	11	5	US-09-641-528-22454	Sequence 22454, A	492	6	1.2	60	5	US-09-978-825-3865	Sequence 3865, Ap
420	6	1.2	11	5	US-09-641-528-22572	Sequence 22572, A	493	6	1.2	60	5	US-09-978-825-3865	Sequence 3865, Ap
421	6	1.2	11	5	US-09-641-528-22735	Sequence 22735, A	494	6	1.2	60	6	US-09-513-999C-6713	Sequence 6713, Ap
422	6	1.2	11	5	US-09-641-528-27725	Sequence 27725, A	495	6	1.2	60	6	US-10-057-498-3865	Sequence 3865, Ap
423	6	1.2	11	5	US-09-641-528-28097	Sequence 28097, A	496	6	1.2	61	1	PCT-US02-32727-9646	Sequence 9646, Ap
424	6	1.2	11	5	US-09-641-528-36069	Sequence 36069, A	497	6	1.2	61	5	US-09-513-999C-6266	Sequence 6266, Ap
425	6	1.2	11	5	US-09-641-528-36407	Sequence 36407, A	498	6	1.2	61	5	US-09-978-825-9646	Sequence 9646, Ap
426	6	1.2	11	5	US-09-641-528A-1154	Sequence 1154, Ap	499	6	1.2	61	5	US-09-864-408A-7754	Sequence 7754, Ap
427	6	1.2	11	5	US-09-641-528A-6038	Sequence 6038, Ap	500	6	1.2	61	5	US-09-513-999C-6266	Sequence 6266, Ap
428	6	1.2	11	5	US-09-641-528A-6103	Sequence 6103, Ap	501	6	1.2	61	6	US-10-057-498-9646	Sequence 9646, Ap
429	6	1.2	11	5	US-09-641-528A-14451	Sequence 14451, A	502	6	1.2	62	1	PCT-US02-32727-1656	Sequence 1656, Ap
430	6	1.2	11	5	US-09-641-528A-14861	Sequence 14861, A	503	6	1.2	62	1	US-09-978-825-1656	Sequence 1656, Ap
431	6	1.2	11	5	US-09-641-528A-22454	Sequence 22454, A	504	6	1.2	62	6	US-10-057-498-1656	Sequence 1656, Ap
432	6	1.2	11	5	US-09-641-528A-22572	Sequence 22572, A	505	6	1.2	62	6	US-10-203-138A-12709	Sequence 12709, A
433	6	1.2	11	5	US-09-641-528A-27725	Sequence 27725, A	506	6	1.2	64	5	US-09-513-999C-6113	Sequence 6113, Ap
434	6	1.2	11	5	US-09-641-528A-28097	Sequence 28097, A	507	6	1.2	64	5	US-09-724-676A-65952	Sequence 65952, A
435	6	1.2	11	5	US-09-641-528A-36069	Sequence 36069, A	508	6	1.2	64	5	US-09-724-676A-65952	Sequence 65952, A
436	6	1.2	11	5	US-09-641-528A-36407	Sequence 36407, A	509	6	1.2	64	5	US-09-513-999C-6113	Sequence 6113, Ap
437	6	1.2	11	5	US-09-641-528A-50701	Sequence 50701, A	510	6	1.2	65	1	PCT-US02-32727-17827	Sequence 17827, A
438	6	1.2	15	5	US-09-641-528A-50701	Sequence 50701, A	511	6	1.2	65	5	US-09-978-825-17827	Sequence 17827, A
439	6	1.2	15	5	US-09-641-528A-50701	Sequence 50701, A	512	6	1.2	65	5	US-10-057-498-17827	Sequence 17827, A
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441	6	1.2	19	6	US-10-030-850-14	Sequence 14, Appl	514	6	1.2	66	5	PCT-US02-32727-15283	Sequence 15283, A
442	6	1.2	20	1	PCT-US02-34021-358	Sequence 358, App	515	6	1.2	67	1	PCT-US02-32727-20738	Sequence 20738, A
443	6	1.2	20	6	US-10-225-567A-861	Sequence 861, App	516	6	1.2	67	5	US-09-978-825-15283	Sequence 15283, A
444	6	1.2	20	6	US-10-280-066-358	Sequence 358, App	517	6	1.2	67	5	US-09-978-825-20738	Sequence 20738, A
445	6	1.2	21	5	US-09-721-708A-107	Sequence 107, App	518	6	1.2	67	6	US-10-057-498-15283	Sequence 15283, A
446	6	1.2	21	5	US-09-721-708A-107	Sequence 107, App	519	6	1.2	67	6	US-10-057-498-20738	Sequence 20738, A
447	6	1.2	21	5	US-10-109-048-926	Sequence 926, App	520	6	1.2	68	5	US-09-513-999C-7136	Sequence 7136, Ap
448	6	1.2	29	6	US-10-306-631-81	Sequence 81, Appl	521	6	1.2	68	5	PCT-US02-32727-13796	Sequence 13796, Ap
449	6	1.2	35	6	US-10-341-200-18	Sequence 18, Appl	522	6	1.2	69	5	US-09-978-825-13796	Sequence 13796, A
450	6	1.2	40	6	US-10-031-167-11	Sequence 11, Appl	523	6	1.2	69	6	US-10-057-498-13796	Sequence 13796, A
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452	6	1.2	47	1	PCT-US02-40655-382	Sequence 382, App	525	6	1.2	72	1	PCT-US02-32727-13629	Sequence 13629, A
453	6	1.2	48	6	US-10-282-122A-44263	Sequence 44263, A	526	6	1.2	72	1	PCT-US02-32727-27291	Sequence 27291, A
454	6	1.2	50	1	PCT-US02-32727-23637	Sequence 23637, A	527	6	1.2	72	5	US-09-978-825-12935	Sequence 12935, A
455	6	1.2	50	5	US-09-978-825-23637	Sequence 23637, A	528	6	1.2	72	5	US-09-978-825-13629	Sequence 13629, A
456	6	1.2	50	6	US-10-057-498-23637	Sequence 23637, A	529	6	1.2	72	5	US-09-978-825-27291	Sequence 27291, A
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458	6	1.2	51	6	US-09-978-825-24818	Sequence 24818, A	531	6	1.2	72	6	US-10-057-498-13629	Sequence 13629, A
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460	6	1.2	52	1	PCT-US02-32727-14560	Sequence 14560, A	533	6	1.2	72	6	US-10-057-498-27291	Sequence 27291, A
461	6	1.2	52	1	PCT-US02-32727-20815	Sequence 20815, A	534	6	1.2	73	1	PCT-US02-32727-23785	Sequence 23785, A
462	6	1.2	52	1	US-09-978-825-9460	Sequence 9460, Ap	535	6	1.2	73	1	PCT-US02-32727-26667	Sequence 26667, A
463	6	1.2	52	5	US-09-978-825-14560	Sequence 14560, A	536	6	1.2	73	1	PCT-US02-30050-64	Sequence 64, Appl
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539	6	1.2	73	6	US-10-057-498-23785	Sequence 23785, A	612	6	1.2	97	6	US-10-057-498-801	Sequence 801, App
540	6	1.2	73	6	US-10-057-498-26667	Sequence 26667, A	613	6	1.2	97	6	US-10-057-498-14364	Sequence 14364, A
541	6	1.2	73	6	US-10-252-948-75	Sequence 75, Appl	614	6	1.2	98	1	PCT-US02-36123-32	Sequence 32, Appl
542	6	1.2	73	6	US-10-156-761-11956	Sequence 11956, A	615	6	1.2	98	1	US-10-203-138A-12470	Sequence 12470, A
543	6	1.2	75	6	US-10-403-340-4	Sequence 4, Appl	616	6	1.2	99	6	US-10-282-122A-51632	Sequence 51632, A
544	6	1.2	75	7	US-60-452-680-15538	Sequence 15538, A	617	6	1.2	100	1	PCT-US02-32727-6106	Sequence 6106, App
545	6	1.2	75	7	US-60-452-680-15539	Sequence 15539, A	618	6	1.2	100	1	PCT-US03-04649-9	Sequence 9, Appl
546	6	1.2	76	1	PCT-US02-32727-848	Sequence 848, App	619	6	1.2	100	5	US-09-978-825-6106	Sequence 6106, App
547	6	1.2	76	1	PCT-US02-32727-30499	Sequence 30499, A	620	6	1.2	100	5	US-09-864-408A-7456	Sequence 7456, App
548	6	1.2	76	5	US-09-978-825-848	Sequence 848, App	621	6	1.2	100	5	US-10-057-498-6106	Sequence 6106, App
549	6	1.2	76	5	US-09-978-825-30499	Sequence 30499, A	622	6	1.2	100	7	US-60-438-000-91	Sequence 91, Appl
550	6	1.2	76	6	US-10-057-498-848	Sequence 848, App	623	6	1.2	100	7	US-60-455-444-6258	Sequence 6258, App
551	6	1.2	77	5	US-09-864-408A-5768	Sequence 5768, App	624	6	1.2	101	1	PCT-US02-32727-23884	Sequence 23884, App
552	6	1.2	77	6	US-10-209-582-900	Sequence 900, App	625	6	1.2	101	1	PCT-US02-32727-30715	Sequence 30715, A
553	6	1.2	77	6	US-10-403-340-5	Sequence 5, Appl	626	6	1.2	101	5	US-09-978-825-23884	Sequence 23884, A
554	6	1.2	78	1	PCT-US02-32727-29042	Sequence 29042, A	627	6	1.2	101	5	US-09-978-825-30715	Sequence 30715, A
555	6	1.2	78	5	US-09-978-825-29042	Sequence 29042, A	628	6	1.2	101	5	US-10-057-498-23884	Sequence 23884, A
556	6	1.2	78	6	US-10-057-498-29042	Sequence 29042, A	629	6	1.2	101	6	US-10-300-616-47	Sequence 47, Appl
557	6	1.2	80	1	PCT-US02-32727-1161	Sequence 1161, App	630	6	1.2	103	5	US-09-724-676-73652	Sequence 73652, A
558	6	1.2	80	1	PCT-US02-32727-2109	Sequence 2109, App	631	6	1.2	103	5	US-09-724-676-73653	Sequence 73653, A
559	6	1.2	80	1	PCT-US02-32727-7715	Sequence 7715, App	632	6	1.2	103	5	US-09-724-676-73654	Sequence 73654, A
560	6	1.2	80	5	US-09-978-825-1161	Sequence 1161, App	633	6	1.2	103	5	US-09-724-676A-73652	Sequence 73652, A
561	6	1.2	80	5	US-09-978-825-2109	Sequence 2109, App	634	6	1.2	103	5	US-09-724-676A-73653	Sequence 73653, A
562	6	1.2	80	5	US-09-978-825-7715	Sequence 7715, App	635	6	1.2	103	5	US-09-724-676A-73654	Sequence 73654, A
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564	6	1.2	80	6	US-10-057-498-2109	Sequence 2109, App	637	6	1.2	104	1	PCT-US02-32727-29965	Sequence 29965, A
565	6	1.2	80	6	US-10-057-498-7715	Sequence 7715, App	638	6	1.2	104	5	US-09-724-676-79428	Sequence 79428, A
566	6	1.2	81	1	PCT-US02-32727-18424	Sequence 18424, A	639	6	1.2	104	5	US-09-724-676A-79428	Sequence 79428, A
567	6	1.2	81	5	US-09-978-825-18424	Sequence 18424, A	640	6	1.2	104	5	US-09-978-825-15857	Sequence 15857, A
568	6	1.2	81	6	US-10-057-498-18424	Sequence 18424, A	641	6	1.2	104	5	US-09-978-825-29965	Sequence 29965, A
569	6	1.2	81	6	US-10-351-334-325	Sequence 325, App	642	6	1.2	104	6	US-10-057-498-15857	Sequence 15857, A
570	6	1.2	82	5	US-09-513-999C-4382	Sequence 4382, App	643	6	1.2	105	5	US-09-864-408A-9050	Sequence 9050, App
571	6	1.2	82	5	US-09-513-999C-4382	Sequence 4382, App	644	6	1.2	105	5	PCT-US02-32727-25943	Sequence 25943, A
572	6	1.2	82	6	US-10-351-334-234	Sequence 234, App	645	6	1.2	106	5	US-09-978-825-25943	Sequence 25943, A
573	6	1.2	83	1	PCT-US02-32727-25149	Sequence 25149, A	646	6	1.2	106	6	US-10-057-498-25943	Sequence 25943, A
574	6	1.2	83	5	US-09-978-825-25149	Sequence 25149, A	647	6	1.2	107	1	PCT-US02-32727-822	Sequence 822, App
575	6	1.2	83	6	US-10-057-498-25149	Sequence 25149, A	648	6	1.2	107	5	US-09-978-825-822	Sequence 822, App
576	6	1.2	83	6	US-10-380-731-852	Sequence 852, App	649	6	1.2	107	6	US-10-057-498-822	Sequence 822, App
577	6	1.2	84	6	US-10-335-977-9188	Sequence 9188, App	650	6	1.2	109	1	PCT-US02-32727-11859	Sequence 11859, A
578	6	1.2	84	7	US-60-453-135-10280	Sequence 10280, A	651	6	1.2	109	1	PCT-US02-32727-14716	Sequence 14716, A
579	6	1.2	84	7	PCT-US02-32727-397	Sequence 397, App	652	6	1.2	109	5	US-09-978-825-11859	Sequence 11859, A
580	6	1.2	85	1	US-09-978-825-397	Sequence 397, App	653	6	1.2	109	5	US-09-978-825-14716	Sequence 14716, A
581	6	1.2	85	5	US-10-057-498-397	Sequence 397, App	654	6	1.2	109	6	US-10-057-498-11859	Sequence 11859, A
582	6	1.2	85	6	US-10-363-936-347	Sequence 347, App	655	6	1.2	109	6	US-10-057-498-14716	Sequence 14716, A
583	6	1.2	87	6	PCT-US02-32727-17909	Sequence 17909, A	656	6	1.2	109	6	US-10-203-138A-10619	Sequence 10619, A
584	6	1.2	88	1	PCT-US02-32727-19296	Sequence 19296, A	657	6	1.2	109	6	US-10-276-781-1377	Sequence 1377, App
585	6	1.2	88	1	PCT-US02-32727-19296	Sequence 19296, A	658	6	1.2	110	1	PCT-US02-32727-23018	Sequence 23018, A
586	6	1.2	88	5	US-09-950-084-7372	Sequence 7372, App	659	6	1.2	110	5	US-09-513-999C-7883	Sequence 7883, App
587	6	1.2	88	5	US-09-978-825-17909	Sequence 17909, A	660	6	1.2	110	5	US-09-978-825-23018	Sequence 23018, A
588	6	1.2	88	5	US-09-978-825-19296	Sequence 19296, A	661	6	1.2	110	5	US-09-513-999C-7883	Sequence 7883, App
589	6	1.2	88	6	US-10-057-498-17909	Sequence 17909, A	662	6	1.2	110	6	US-10-057-498-23018	Sequence 23018, A
590	6	1.2	88	6	US-10-057-498-19296	Sequence 19296, A	663	6	1.2	110	6	US-10-309-629-8	Sequence 8, Appl
591	6	1.2	89	6	US-10-277-802-76	Sequence 76, Appl	664	6	1.2	111	6	US-10-335-977-9189	Sequence 9189, App
592	6	1.2	89	6	US-10-282-122A-65530	Sequence 65530, A	665	6	1.2	112	1	PCT-US02-32727-21993	Sequence 21993, App
593	6	1.2	89	6	US-10-282-122A-65698	Sequence 65698, A	666	6	1.2	112	5	US-09-978-825-21993	Sequence 21993, A
594	6	1.2	89	6	US-10-282-122A-76751	Sequence 76751, A	667	6	1.2	112	6	US-10-057-498-21993	Sequence 21993, A
595	6	1.2	92	6	US-10-094-886A-194	Sequence 194, App	668	6	1.2	112	6	US-10-156-761-12166	Sequence 12166, A
596	6	1.2	92	6	US-10-094-886A-194	Sequence 194, App	669	6	1.2	113	5	US-09-949-016-7586	Sequence 7586, App
597	6	1.2	95	1	PCT-US02-32727-3990	Sequence 3990, App	670	6	1.2	113	5	US-10-282-122A-57655	Sequence 57655, A
598	6	1.2	95	1	PCT-US02-32727-28407	Sequence 28407, A	671	6	1.2	114	5	US-09-724-676-86956	Sequence 86956, A
599	6	1.2	95	5	US-09-724-676-83238	Sequence 83238, A	672	6	1.2	114	5	US-09-724-676-86957	Sequence 86957, A
600	6	1.2	95	5	US-09-724-676A-83238	Sequence 83238, A	673	6	1.2	114	5	US-09-724-676A-86957	Sequence 86957, A
601	6	1.2	95	5	US-09-978-825-3990	Sequence 3990, App	674	6	1.2	114	5	PCT-US02-32727-30846	Sequence 30846, A
602	6	1.2	95	5	US-09-978-825-28407	Sequence 28407, A	675	6	1.2	115	5	US-09-978-825-30846	Sequence 30846, A
603	6	1.2	95	6	US-10-057-498-3990	Sequence 3990, App	676	6	1.2	115	5	US-09-864-408A-7730	Sequence 7730, App
604	6	1.2	95	6	US-10-057-498-28407	Sequence 28407, A	677	6	1.2	115	5	US-10-264-237-1496	Sequence 1496, App
605	6	1.2	96	6	US-10-333-610-13	Sequence 13, Appl	678	6	1.2	115	6	US-10-276-781-1129	Sequence 1129, App
606	6	1.2	97	1	PCT-US02-32727-801	Sequence 801, App	679	6	1.2	115	6	US-10-351-334-324	Sequence 324, App
607	6	1.2	97	1	PCT-US02-32727-14364	Sequence 14364, A	680	6	1.2	115	6	PCT-US02-32727-9004	Sequence 9004, App
608	6	1.2	97	1	PCT-US02-32727-29917	Sequence 29917, A	681	6	1.2	117	5	US-09-978-825-9004	Sequence 9004, App
609	6	1.2	97	5	US-09-978-825-801	Sequence 801, App	682	6	1.2	117	5	US-10-057-498-9004	Sequence 9004, App
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585	1.2	118	5	US-09-724-676A-59394	Sequence 59394, A	758	6	1.2	151	5	US-09-675-784A-9833	Sequence 9833, Ap
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976 6 1.2 226 6 US-10-187-749-122 Sequence 122, App
977 6 1.2 226 6 US-10-218-140-6062 Sequence 6062, App
978 6 1.2 226 6 US-10-199-672-122 Sequence 122, App
979 6 1.2 226 6 US-10-194-486-122 Sequence 122, App
980 6 1.2 227 6 US-10-366-683-28099 Sequence 28099, A
981 6 1.2 227 6 US-10-282-122A-63761 Sequence 63761, A
982 6 1.2 227 6 US-10-156-761-10575 Sequence 10575, A
983 6 1.2 228 6 US-10-156-761-10575 Sequence 10575, A
984 6 1.2 230 1 PCT-US02-32727-13771 Sequence 13771, A
985 6 1.2 230 5 US-09-978-825-13771 Sequence 13771, A
986 6 1.2 230 6 US-10-057-498-13771 Sequence 13771, A
987 6 1.2 231 6 US-10-369-493-8364 Sequence 8364, App
988 6 1.2 232 5 US-09-724-676-64863 Sequence 64863, A
989 6 1.2 232 5 US-09-724-676A-64863 Sequence 64863, A
990 6 1.2 233 1 PCT-US02-36123-3044 Sequence 3044, App
991 6 1.2 233 6 US-10-282-122A-74685 Sequence 74685, A
992 6 1.2 234 5 US-09-724-676-64898 Sequence 64898, A
993 6 1.2 234 5 US-09-724-676A-64898 Sequence 64898, A
994 6 1.2 234 6 US-10-366-683-17302 Sequence 17302, A
995 6 1.2 234 6 US-10-289-762-241 Sequence 241, App
996 6 1.2 236 6 US-10-276-774-2408 Sequence 2408, App
997 6 1.2 236 6 US-10-282-122A-57603 Sequence 57603, A
998 6 1.2 237 6 US-10-264-237-1929 Sequence 1929, App
999 6 1.2 238 6 US-10-282-122A-72127 Sequence 72127, A
1000 6 1.2 238 6 US-10-369-493-757 Sequence 757, App

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ALIGNMENTS

```

RESULT 1
US-10-266-252-5
; Sequence 5, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-5

```

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Query Match 100.0%; Score 500; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLVLVLEAARALSPQAGHDEGPGSGWAAGTVRGWNRRARSPGHVSEPD 60
Db 1 MRGELWLVLVLEAARALSPQAGHDEGPGSGWAAGTVRGWNRRARSPGHVSEPD 60

QY 61 TQSLDGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANSQVK 120
Db 61 TQSLDGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANSQVK 120

QY 121 IHTILSNTHRAQSRVLSDFDPFYCHPLRQITATGGTFPMGDVIHRLMTATQYVAPLMA 180
Db 121 IHTILSNTHRAQSRVLSDFDPFYCHPLRQITATGGTFPMGDVIHRLMTATQYVAPLMA 180

QY 181 NFNEGYSDNSTVYFDNGTVFVQMDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNEGYSDNSTVYFDNGTVFVQMDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240

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QY 181 NFNPGYSDNSTVYFDNGTVFVQMDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPGYSDNSTVYFDNGTVFVQMDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240

QY 241 SVPEISSQHPVKTKGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMSAVEFTP 300
Db 241 SVPEISSQHPVKTKGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMSAVEFTP 300

QY 301 LPTCLOHRSKCDACMSDDLTFNCSWCHVLRQSSGDFDRYQEWMDYGCQAQEAEGRMCEDFQ 360
Db 301 LPTCLOHRSKCDACMSDDLTFNCSWCHVLRQSSGDFDRYQEWMDYGCQAQEAEGRMCEDFQ 360

QY 361 DEHDHSDSPDTSFSPYDGLTDTSSSLFTDLSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Db 361 DEHDHSDSPDTSFSPYDGLTDTSSSLFTDLSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420

QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480

QY 481 YAEVPSGHEKEGFMEEAEOC 500
Db 481 YAEVPSGHEKEGFMEEAEOC 500

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RESULT 2

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US-10-266-252-15
; Sequence 15, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-15

```

```

Query Match 100.0%; Score 500; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRGELWLVLVLEAARALSPQAGHDEGPGSGWAAGTVRGWNRRARSPGHVSEPD 60
Db 1 MRGELWLVLVLEAARALSPQAGHDEGPGSGWAAGTVRGWNRRARSPGHVSEPD 60

QY 61 TQSLDGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANSQVK 120
Db 61 TQSLDGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANSQVK 120

QY 121 IHTILSNTHRAQSRVLSDFDPFYCHPLRQITATGGTFPMGDVIHRLMTATQYVAPLMA 180
Db 121 IHTILSNTHRAQSRVLSDFDPFYCHPLRQITATGGTFPMGDVIHRLMTATQYVAPLMA 180

QY 181 NFNEGYSDNSTVYFDNGTVFVQMDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNEGYSDNSTVYFDNGTVFVQMDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240

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QY 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
|||||
DB 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQ 360
|||||
DB 301 LPTCLQHRSCDACMSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
|||||
DB 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480
|||||
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMFAEQC 500
|||||
DB 481 YAEVPSGHEKEGFMFAEQC 500

RESULT 3
US-60-453-135-13631
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13631
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13631
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Query Match 100.0%; Score 500; DB 7; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
|||||
DB 1 MRGELWLLVLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
|||||
DB 61 TQSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVVLSDFDPFYGHPLRQITATGGFIFMGDVYIHRMLTATQYVAPLMA 180
|||||
DB 121 IHTILSNTHROASRVVLSDFDPFYGHPLRQITATGGFIFMGDVYIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYVFDNGTVFVQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
|||||
DB 181 NFNPGYSDNSTVYVFDNGTVFVQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
|||||
DB 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQ 360
|||||
DB 301 LPTCLQHRSCDACMSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
|||||
DB 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
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RESULT 5

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US-10-266-252-3
; Sequence 3, Application US/10266252
; GENERAL INFORMATION:
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QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480
|||||
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMFAEQC 500
|||||
DB 481 YAEVPSGHEKEGFMFAEQC 500

RESULT 4
US-60-453-050-13631
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13631
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13631
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Query Match 100.0%; Score 500; DB 7; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
|||||
DB 1 MRGELWLLVLLVLRRAARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
QY 61 TQSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
|||||
DB 61 TQSQDLGGGTAMDTLPDNRTRVVEDNHSYVSRLYGSPSEPHSRELWVDVAEANRSQVK 120
QY 121 IHTILSNTHROASRVVLSDFDPFYGHPLRQITATGGFIFMGDVYIHRMLTATQYVAPLMA 180
|||||
DB 121 IHTILSNTHROASRVVLSDFDPFYGHPLRQITATGGFIFMGDVYIHRMLTATQYVAPLMA 180
QY 181 NFNPGYSDNSTVYVFDNGTVFVQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
|||||
DB 181 NFNPGYSDNSTVYVFDNGTVFVQWDHYVLOGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
|||||
DB 241 SVPEISSQHPVKTLGSDAFMILNPSDPVPSRRRSIFEXHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQ 360
|||||
DB 301 LPTCLQHRSCDACMSSDLTFCNSCHVLQRCSSGFDRYQEWMDYGCQAQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
|||||
DB 361 DEDHDSASPDTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480
|||||
DB 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAALFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMFAEQC 500
|||||
DB 481 YAEVPSGHEKEGFMFAEQC 500
```

; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3:
; LENGTH: 527
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-3

Query Match 100.0%; Score 500; DB 6; Length 527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRGELWLLVLRRAALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSPDR 60
Db 28 MRGELWLLVLRRAALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSPDR 87
Qy 61 TQLSQDLGGGTAMDTLTPDNTRRVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVK 120
Db 88 TQLSQDLGGGTAMDTLTPDNTRRVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVK 147
Qy 121 IHTILSNTHROASRVLSDFPPFYGHPLROITATGGFIEMGDVIRHMLTATQYVAPLMA 180
Db 148 IHTILSNTHROASRVLSDFPPFYGHPLROITATGGFIEMGDVIRHMLTATQYVAPLMA 207
Qy 181 NFNPYSDNSTVYFDNGTVFVQWQDHVYLQGWEDKGSFTFQALHHDGRIVFAYKEIPM 240
Db 208 NFNPYSDNSTVYFDNGTVFVQWQDHVYLQGWEDKGSFTFQALHHDGRIVFAYKEIPM 267
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMASVEFTP 300
Db 268 SVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMASVEFTP 327
Qy 301 LPTCLOHRSQDACMSDLTFNCSCWCHVLRCSGDFRYRQEWMDYGCQAEGRMCEDEQ 360
Db 328 LPTCLOHRSQDACMSDLTFNCSCWCHVLRCSGDFRYRQEWMDYGCQAEGRMCEDEQ 387
Qy 361 DEDHDSASPTSFSPYDGLTTSSSLFIDSLTDDTTLNYPYAGDGLQNNLSPKTKGT 420
Db 388 DEDHDSASPTSFSPYDGLTTSSSLFIDSLTDDTTLNYPYAGDGLQNNLSPKTKGT 447
Qy 421 PVHLGTIVGIVLAVLLVAAILIAGIYNGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 480
Db 448 PVHLGTIVGIVLAVLLVAAILIAGIYNGHPTSNAAALFFIERRPHHPWPKFRSHPDHST 507
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 508 YAEVPSGHEKEGFMEAEQC 527

RESULT 6
US-10-266-252-8
; Sequence 8, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 482
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-8

Query Match 96.4%; Score 482; DB 6; Length 482;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 19 LSPQPCAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTLP 78
Db 1 LSPQPCAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPDRTQLSQDLGGGTAMDTLP 60
Qy 79 DNTRRVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROASRVVLS 138
Db 61 DNTRRVEDNHSYVSRLYGPSEPHSRELWVDVAEANSQVKIHTILSNTHROASRVVLS 120
Qy 139 FDFPFYGHPLROITATGGFIEMGDVIRHMLTATQYVAPLMAFNPNPGYSDNSTVYFDNG 198
Db 121 FDFPFYGHPLROITATGGFIEMGDVIRHMLTATQYVAPLMAFNPNPGYSDNSTVYFDNG 180
Qy 199 TVFVQWQDHVYLQGWEDKGSFTFQALHHDGRIVFAYKEIPMSVPEISSQHPVKTKGLSD 258
Db 181 TVFVQWQDHVYLQGWEDKGSFTFQALHHDGRIVFAYKEIPMSVPEISSQHPVKTKGLSD 240
Qy 259 AFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMASVEFTPCTCLOHRSQDACMSDL 318
Db 241 AFMILNPSDPVPESSRRSIFEFYHRIELDPKSVTSMASVEFTPCTCLOHRSQDACMSDL 300
Qy 319 TFNCSCWCHVLRCSGDFRYRQEWMDYGCQAEGRMCEDEQDEHDSASPTSFSPYDG 378
Db 301 TFNCSCWCHVLRCSGDFRYRQEWMDYGCQAEGRMCEDEQDEHDSASPTSFSPYDG 360
Qy 379 DLTTTSSSLFIDSLTDDTTLNYPYAGDGLQNNLSPKTKGTPVHLGTIVGIVLAVLLVA 438
Db 361 DLTTTSSSLFIDSLTDDTTLNYPYAGDGLQNNLSPKTKGTPVHLGTIVGIVLAVLLVA 420
Qy 439 AILLAGIYNGHPTSNAAALFFIERRPHHPWPKFRSHPDHSTYAEVPSGHEKEGFMEAE 498
Db 421 AILLAGIYNGHPTSNAAALFFIERRPHHPWPKFRSHPDHSTYAEVPSGHEKEGFMEAE 480
Qy 499 QC 500
Db 481 QC 482

RESULT 7
US-60-453-135-13630
; Sequence 13630, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13630
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13630

Query Match 85.4%; Score 427; DB 7; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 MDLPDNRTRVVDNHSYVSRSLYGPSEPHSRELWVDVAEARNRQVKIHTILSNTHROAS 133
DB 1 MDLPDNRTRVVDNHSYVSRSLYGPSEPHSRELWVDVAEARNRQVKIHTILSNTHROAS 60
QY 134 RVLSDFDPFGYHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVV 193
DB 61 RVLSDFDPFGYHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVV 120
QY 194 YFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVK 253
DB 121 YFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVK 180
QY 254 TGLSDAFMILNPSDPVPSRRRSIFEXHRIELDPKSVTSMASAVEFTPLPTCLQHRSCDAC 313
DB 181 TGLSDAFMILNPSDPVPSRRRSIFEXHRIELDPKSVTSMASAVEFTPLPTCLQHRSCDAC 240
QY 314 MSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPTSF 373
DB 241 MSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPTSF 300
QY 374 SPYDGLTTSSSLFTDLSLTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTIVGIVLA 433
DB 301 SPYDGLTTSSSLFTDLSLTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTIVGIVLA 360
QY 434 VLLVAAILLAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEG 493
DB 361 VLLVAAILLAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEG 420
QY 494 FMEAEQC 500
DB 421 FMEAEQC 427

RESULT 8
US-60-453-050-13630
; Sequence 13630, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453.050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13630
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13630

Query Match 85.4%; Score 427; DB 7; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 MDLPDNRTRVVDNHSYVSRSLYGPSEPHSRELWVDVAEARNRQVKIHTILSNTHROAS 133
DB 1 MDLPDNRTRVVDNHSYVSRSLYGPSEPHSRELWVDVAEARNRQVKIHTILSNTHROAS 60
QY 134 RVLSDFDPFGYHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVV 193

DB 61 RVLSDFDPFGYHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVV 120
QY 194 YFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVK 253
DB 121 YFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVK 180
QY 254 TGLSDAFMILNPSDPVPSRRRSIFEXHRIELDPKSVTSMASAVEFTPLPTCLQHRSCDAC 313
DB 181 TGLSDAFMILNPSDPVPSRRRSIFEXHRIELDPKSVTSMASAVEFTPLPTCLQHRSCDAC 240
QY 314 MSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPTSF 373
DB 241 MSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGRMCEDFQDEHDSASPTSF 300
QY 374 SPYDGLTTSSSLFTDLSLTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTIVGIVLA 433
DB 301 SPYDGLTTSSSLFTDLSLTEDDTKLNYPAGDGLQNNLSPKTKGTPVHLGTIVGIVLA 360
QY 434 VLLVAAILLAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEG 493
DB 361 VLLVAAILLAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEG 420
QY 494 FMEAEQC 500
DB 421 FMEAEQC 427

RESULT 9
US-10-266-252-10

; Sequence 10, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyang
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 488
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-10

Query Match 79.0%; Score 395; DB 6; Length 488;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLVLRREARALSPQCGAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
DB 1 MRGELWLLVLVLRREARALSPQCGAGHDEGPGSGWAAKGTVRGNRRRARESPGHVSEPD 60
QY 61 TQLSQDGGGTLMADTLPDNRTRVVDNHSYVSRSLYGPSEPHSRELWVDVAEARNRQV 120
DB 61 TQLSQDGGGTLMADTLPDNRTRVVDNHSYVSRSLYGPSEPHSRELWVDVAEARNRQV 120
QY 121 IHTILSNTHROASRVLSDFDPFGYHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180
DB 121 IHTILSNTHROASRVLSDFDPFGYHPLRQITATGGFIFMGDVIHRMLTATQVAPLMA 180
QY 181 NFNPYSDNSTVVYFDNGTVFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240

Db 181 NFNPGYSDNSTVVFVQDNGTVFVQWHDVHYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASAVEFTP 300
Db 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASAVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFNCWCHVLQRCSSGFDRIYQWMDYGAQAEGRMCEDFQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCWCHVLQRCSSGFDRIYQWMDYGAQAEGRMCEDFQ 360
QY 361 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLLTE 395
Db 361 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLLTE 395
RESULT 10
US-10-266-252-12
; Sequence 12, Application US/10266252
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Ren, Feiyan
; TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides and Therapeutic Uses Thereof
; FILE REFERENCE: HYS-44A
; CURRENT APPLICATION NUMBER: US/10/266,252
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327,731
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 470
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-266-252-12

Query Match 75.4%; Score 377; DB 6; Length 470;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 LSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSDLGCGGTAMDTP 78
Db 1 LSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPDRTQLSDLGCGGTAMDTP 60
QY 79 DNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVKTHILSNTHROASRWVLS 138
Db 61 DNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVKTHILSNTHROASRWVLS 120
QY 139 FDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMANFNPGYSDNSTVVFVQDNG 198
Db 121 FDFPFYGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMANFNPGYSDNSTVVFVQDNG 180
QY 199 TVFVQWHDVHYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKGLSD 258
Db 181 TVFVQWHDVHYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTKGLSD 240
QY 259 AFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASAVEFTPPLTCLQHRSCDACMSSDL 318
Db 241 AFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASAVEFTPPLTCLQHRSCDACMSSDL 300
QY 319 TFNCWCHVLQRCSSGFDRIYQWMDYGAQAEGRMCEDFQDEHDSASPDTSFSPYDG 378
Db 301 TFNCWCHVLQRCSSGFDRIYQWMDYGAQAEGRMCEDFQDEHDSASPDTSFSPYDG 360
QY 379 DLTTSSSLFIDSLLTE 395
Db 361 DEDHDSASPDTSFSPYDGLTFTSSSLFIDSLLTE 395

Db 361 DLTTSSSLFIDSLLTE 377
RESULT 11
US-10-218-140-5790
; Sequence 5790, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curanator Version 1.0
; SEQ ID NO 5790
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)...(1)
; OTHER INFORMATION: "Xaa" = "Any Amino Acid"
US-10-218-140-5790

Query Match 74.2%; Score 371; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 60
Db 29 MRGELWLLVLRARALSPQAGHDEGPGSGWAAGTGVGNRRRARESPGHVSEPD 88
QY 61 TOLSDQLGGGTAMDTPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVK 120
Db 89 TOLSDQLGGGTAMDTPDNRTRVVEDNHSYVSRLYGSPHSELWVDVAEANRSQVK 148
QY 121 IHTILSNTHROASRWVLSFDPFPGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMA 180
Db 149 IHTILSNTHROASRWVLSFDPFPGHPLRQITATGGFIEMGDVTHRMLTATQVAPLMA 208
QY 181 NFNPGYSDNSTVVFVQDNGTVFVQWHDVHYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPM 240
Db 209 NFNPGYSDNSTVVFVQDNGTVFVQWHDVHYLQGWEDKSGFTFOAALHHDGRIVFAYKEIPM 268
QY 241 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASAVEFTP 300
Db 269 SVPEISSQHPVKTKGLSDAFMLNPSDPVPSRRRSIFEXHRIELDPKVTSMASAVEFTP 328
QY 301 LPTCLQHRSCDACMSSDLTFNCWCHVLQRCSSGFDRIYQWMDYGAQAEGRMCEDFQ 360
Db 329 LPTCLQHRSCDACMSSDLTFNCWCHVLQRCSSGFDRIYQWMDYGAQAEGRMCEDFQ 388
QY 361 DEDHDSASPD 371
Db 389 DEDHDSASPD 399
RESULT 12
US-10-284-237-2453
; Sequence 2453, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAL31PI1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2453
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: MISC_FEATURE
LOCATION: (135)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (141)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2453

Query Match 26.0%; Score 130; DB 6; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.5e-121;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 MDYCAQFAEGRMCEQDEHDSASPTSFSPYDGDLLTTSSSLFDTSLTDDTKLNP 402
|||||
DB 1 MDYCAQFAEGRMCEQDEHDSASPTSFSPYDGDLLTTSSSLFDTSLTDDTKLNP 60
QY 403 YAGDGLQNNLSPTKGTGPHLGTIVGIVLAVLLVAAILAGIYINGHPTSNALFFIER 462
|||||
DB 61 YAGDGLQNNLSPTKGTGPHLGTIVGIVLAVLLVAAILAGIYINGHPTSNALFFIER 120
QY 463 RPHHPAMKF 472
|||||
DB 121 RPHHPAMKF 130

RESULT 13
US-10-266-252-7
Sequence 7, Application US/10266252
GENERAL INFORMATION:
APPLICANT: Ghosh, Malabika
APPLICANT: Tang, Y. Tom
APPLICANT: Ren, Feiyan
TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
FILE REFERENCE: HYS-44A
CURRENT APPLICATION NUMBER: US/10/266,252
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/327,731
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/127,636
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 18
TYPE: PRT
ORGANISM: homo sapiens
US-10-266-252-7

Query Match 3.6%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRRAA 18

DB 1 MRGELWLLVLRRAA 18
|||||

RESULT 14
US-10-266-252-13
Sequence 13, Application US/10266252
GENERAL INFORMATION:
APPLICANT: Ghosh, Malabika
APPLICANT: Tang, Y. Tom
APPLICANT: Ren, Feiyan
TITLE OF INVENTION: Methods And Materials Relating To Stem Cell Growth Factor-Like
FILE REFERENCE: HYS-44A
CURRENT APPLICATION NUMBER: US/10/266,252
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/327,731
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 17
TYPE: PRT
ORGANISM: homo sapiens
US-10-266-252-13

Query Match 3.4%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 IVGIVLAVLLVAAILA 443
|||||
DB 1 IVGIVLAVLLVAAILA 17

RESULT 15
US-10-218-140-526
Sequence 526, Application US/10218140
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: 15966-543 CON
CURRENT APPLICATION NUMBER: US/10/218,140
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/540,763
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/127,728
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/127,636
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 60/127,607
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 6322
SOFTWARE: Curanator Version 1.0
SEQ ID NO 526
LENGTH: 290
TYPE: PRT
ORGANISM: Homo sapiens
US-10-218-140-526

Query Match 2.0%; Score 10; DB 6; Length 290;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146

Db 161 LSFDFEYGH 170
|||||

Search completed: April 22, 2003, 16:24:15
Job time : 101 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:04:50 ; Search time 21 Seconds
(without alignments)
2288.915 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELWLLVLVLEAREALS.....YAEVPSGHEKEGMEABQC 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	611	22.7	476	T19786	hypothetical prote
2	126	4.7	1161	S31213	nidogen precursor
3	115.5	4.3	1568	T09074	semaphorin recepto
4	103.5	3.8	979	C86446	probable cellulose
5	101.5	3.8	743	T09173	EH domain protein
6	101	3.8	733	E86345	hypothetical prote
7	100	3.7	535	S18606	phosphoenolpyruvat
8	99	3.7	1133	T12529	hypothetical prote
9	98	3.6	345	T16074	hypothetical prote
10	98	3.6	1502	S45429	probable membrane
11	97	3.6	708	T83196	NEDD-4 ORF - mouse
12	96.5	3.6	397	S33415	corticosteroid-bin
13	96.5	3.6	679	T19703	hypothetical prote
14	95.5	3.5	399	S71480	homeotic protein H
15	95.5	3.5	887	T70642	ubiquitin ligase N
16	95.5	3.5	2120	T30243	alpha tectorin - C
17	94	3.5	774	JC7265	neprilysin (EC 3.4
18	93.5	3.5	979	JC2349	protein-tyrosine-p
19	93.5	3.5	996	T48721	PTP 35 protein - m
20	93.5	3.5	1977	S54771	sodium channel alp
21	93	3.5	491	AG3506	phosphoenolpyruvat
22	93	3.5	1085	S55352	IFH1 protein - yea
23	92.5	3.4	441	JC7653	pectate lyase (EC
24	92.5	3.4	852	T85041	probable receptor
25	91.5	3.4	614	A98241	hypothetical prote
26	91.5	3.4	614	F86088	hypothetical prote
27	91.5	3.4	810	P2WMBB	2a protein - broad
28	91.5	3.4	1042	A57534	mucin 5AC (clone L
29	91	3.4	633	S47144	mating type A prot

ALIGNMENTS

RESULT 1

T19786

hypothetical protein C36E8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T19786

R:Wilkinson, J.: Barlow, K.

submitted to the EMBL Data Library, August 1994

A:Reference number: Z19177

A:Accession: T19786

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-476 <WIL>

A:Cross-references: EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C36E8.3

A:Experimental source: clone C36E8

C:Genetics:

A:Gene: CESP:C36E8.3

A:Map position: 3

A:Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2

C:Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match	22.7%	Score 611;	DB 2;	Length 476;
Best Local Similarity	34.2%	Pred. No. 3.7e-42;		
Matches 149;	Conservative 65;	Mismatches 160;	Indels 62;	Gaps 15;
QY	46	RRARESPGHVSEPDRTOLS-----QDLGGGTGLAMDTLPDNRTRVVEDNHSYVSRLYGPS	100	
Db	62	RTARAAP-----IPKRSLSAEQDEDEIDPATATIP--PDVEKNDMIDHQYQAEFTVGD	115	
QY	101	EPHSRELVDVAEANSQVKI-----HTILSNTHRQASRVVLSPDFPFYGHPLRQITTIATG	156	
Db	116	GETLKYWINVEQFMKKPRAVGNTPHLLSQSYRRVAVGARLQFKPFYGHKNSNLTATG	175	
QY	157	GFIFMGDVIHRMLTATQYVAPLANENPGYSNDSTVYVDNGTVFVQNDHVVLOGWEOK	216	
Db	176	GFYIGDHSNHLAAQYIAPLMANFHT--YLNNSNLIVADGGEFVVEWRNVOLKEDKDE	234	
QY	217	GSFTFOAALHHDGRVFAYKEIPMSVPEISSQHPVKTKGLSDAFMLN--PSPDVPESRR	274	
Db	235	HSFTFTQILKHGNDIVFIYKDPYDISNIDANHPVKLGISDAYMEKHNHQAAPV--K	291	
QY	275	RSIFEXHRIELDP SKVTSMSAVEFTPLPTCLQHRSCDACMSDLT-FNCSWCHVLQR---	330	
Db	292	RVIVYHRIEIAAKIVSNWTWILKAQPTCISFDTCTNATLPHFNCILWCHAKKSHGG	351	
QY	331	--CS--SGFDRYQEWMDYGCQAEGRMCE-DFQDEHDHSAS-PDTSFSPYDGLTTTS	384	
Db	352	PFCTDEAGLHRRRHQHWFEQNGYQRSKALYCDADDEDEYDEEDYPKSQLMPNGGH---	408	
QY	385	SSLFIDSILTTTDDTKLNPYAGGDCGLONNLSPKTKGTPTVHLGTIVGIVLAVLLVAAILAG	444	
Db	409	LPLDADRMKTKDTTSDSDSEWKGHKKEEPK-----	442	

protein-tyrosine-p
pregnancy-specific
zona pellucida gly
pristinamycin I sy
phosphoenolpyruvat
phosphoenolpyruvat
hypothetical prote
protein tyrosine p
hypothetical prote
hypothetical prote
protein-tyrosine k
Doc4 protein, stre
pregnancy-specific
osteonidogen - hum
probable polyketid
sodium channel pro

QY 445 IYINGHP--TSNAALF 458
 : : : : :
 Db 443 VATTAPVGTQAATF 458

RESULT 2

S31213

nidogen precursor - sea squirt (Halocynthia roretzi)

N:Alternate names: entactin

C:Species: Halocynthia roretzi

C:Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 16-Jun-2000

C:Accession: S31213

R:Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.

Eur. J. Biochem. 213, 11-19, 1993

A:Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of

A:Reference number: S31213; MUID:93238676; PMID:8477687

A:Accession: S31213

A:Molecule type: mRNA

A:Residues: 1-1161 <NAK>

C:Superfamily: EMBL:D14038; NID:g217363; PIDN:BAA03127.1; PID:g217364

C:Keywords: Ascidian nidogen; EGF homology; LDL receptor WYTD-containing repeat homol

F:1-20/Domain: signal sequence <status predicted> <SIG>

F:21-1161/Product: nidogen <status predicted> <NAK>

F:274-306/Domain: EGF homology <EG1>

F:560-574/Region: 3-residue repeats (R-P-V)

F:603-673/Domain: thyroglobulin type I repeat homology <THY1>

F:686-748/Domain: thyroglobulin type I repeat homology <THY2>

F:752-819/Domain: thyroglobulin type I repeat homology <THY3>

F:900-943/Domain: LDL receptor WYTD-containing repeat homology <YWL>

F:944-986/Domain: LDL receptor WYTD-containing repeat homology <YW2>

F:987-1031/Domain: LDL receptor WYTD-containing repeat homology <YW3>

F:1032-1075/Domain: LDL receptor WYTD-containing repeat homology <YW4>

F:1076-1114/Domain: LDL receptor WYTD-containing repeat homology <YW5>

F:1129-1158/Domain: EGF homology <EG2>

F:107,334,360,484/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 4.7%; Score 126; DB 1; Length 1161;

Matches 64; Conservative 34; Mismatches 88; Indels 86; Gaps 12;

QY 137 LSFDPFPGHPLRQITATGGFIEM-----GDVHRMLTATQYVAPLMAN----- 181

Db 47 LSPMTVFYDQYDSVTHTDGFITLNVGADTDCGVL-----LAPMSDLDTPLSG 97

QY 182 --FNPFGSDNSTVY-----FDNCTVFVQWDHVLQGWEDKGSFTFQAA 224

Db 98 DFFREHKDNATIRANTDVREAFIETAGDFNAGSVFVVTWVKYQSASREDGVFTFQCI 157

QY 225 LHHGGRIVFA--YKEIPMSVPEIS---SSQHPVKTGLSDA---FMILNPSF---DV 269

Db 158 VATDGAATFAFLYPQGLAVGENAVKGVNREVTARAGFNDGGREQLLEILSADLLGGDN 217

QY 270 PESRRSIFVHRIELDPSKVTMSAVEFTPLPTCLQHRSCDACMSSDITFNCISWCHVLQ 329

Db 218 AGSOGQIFQIGGLMNNDEASKESK-----KH-----HVKK 249

QY 330 RCSGSDFRYQEW-MDYCCQAQAE-GRMCEDF 359

Db 250 TRQSGFQVSEVNFEDFNIDLEACGPGPCSDF 281

RESULT 3

T09074

semaphorin receptor VESPR - human

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: T09074

R:ComEAU, M.R.; Johnson, R.; DuBose, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; F

Immunity 8, 473-482, 1998

A:Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and b

A:Reference number: Z16555; MUID:98246049; PMID:9586637

A:Accession: T09074

A:Status: preliminary; translated from GB/EMBL/DDBT

A:Molecule type: mRNA

A:Residues: 1-1568 <COM>

A:Cross-references: EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3176762

A:Experimental source: tissue type foreskin; cell type fibroblast

C:Genetics:

A:Gene: VESPR

C:Keywords: receptor; signal transduction

Query Match 4.3%; Score 115.5; DB 2; Length 1568;

Best Local Similarity 20.6%; Pred. No. 0.98;

Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

QY 39 GTVGRNRRRARESPGHVSEPDRT---QLSODLGGGTLMADTLPDNRTRVEDNHSYVVS 94

Db 256 GAATGWPSPMAR-----TAOSTEVLFOGQASLDCGHGH-----PDGR-----R 292

QY 95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 139

Db 293 LLLSSSLVEALDYWAGVFSAAAGEGOERRSPPTTALCLFMSLQAKRVSWDFKTAES 352

QY 140 ----DFPYGHPRLQITATGGFIEMGVHRLMTATQYVAPLMANFNGYSDNSTVYV 194

Db 353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVM-----NRTVLF 391

QY 195 FDNCTVFVQWDHVLQGWEDKGSFTFQAAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249

Db 392 LSGT-----DGQLKVLGENTLSCNPEVVEIKEE 422

QY 250 HPVKTGLSDFAMLLNPDVPSRRRSIFEYHRIELDPKSVTMSAVEFTPLPTCLQHR 309

Db 423 TPV-----FYKLVPDP-----VKNIIYI-----LTAGREVRRIRVANCKHKS 460

QY 310 CDACMSDDLTFNCISWCHVLQRCSSGDFRYQE---WMDYGCQAQAEGRMCEDFQ----D 361

Db 461 CSECLTA-TDPCGCHSLQRCFTFGDCVHSENLENWLDI-----SSGAKKCPKIQIRSS 515

QY 362 EDHDSASPDTSFSP 375

Db 516 KEKTVTVTVMGVSFSP 529

RESULT 4

C86446

probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: C86446

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: C86446

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-979 <STO>

A:Cross-references: GB:AE005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 3.8%; Score 103.5; DB 2; Length 979;

Best Local Similarity 21.2%; Pred. No. 5;

Matches 87; Conservative 48; Mismatches 167; Indels 109; Gaps 19;

QY 4 ELWLVLVLRRAARALSPQAGHDGPGCGAAKGTVRGNRRRARESPGHVSEPDRTQL 63

Db 342 EKXKHKVYVEDQIKERPAL---VAPKATWMSDGT--HWPGTWVWYSGPHSRGDHASV 396
QY 64 SDDL-----GGGTAMD-----TLPDNRTVRVEDNHSYVYVSRLYGPSEPHSR 105
Db 397 IQVLLDPGDPVEGKGGRALDLEGVDIRLP-----MLVYVSRREKRPYDHNK 446
QY 106 ELWVDVAENRSOVKTHITLSTHTRQASRVLSFDPPYGHPLQITATIGGTFMGDVI 165
Db 447 K-----AGAMNALVRASAIMS-----GPFILNDCDHVYNSRAF-----ROGICFMMDHD 493
QY 166 HRMLTATQY-----VAPLMANFNPGYS-----NSTVYV-F 195
Db 494 GDRSVYVQPPQFEGIDPSDRYANKNTVFEDINLRALDIOGPMYVGTGCLFRRTALYGF 553
QY 196 DNGTVFVQVWDHIVYLOQWEDKSGFTFOALHHDGRIVFAYKEIPMSV---PEISSQHUP- 251
Db 554 NPPDVVFE-----EPSPGSCFP-----LIKKRSPATVASEPEYTYDEDR 595
QY 252 -----VKTGLSDAFMLNPSDPVPSRRSIFEXH--RIELDPKSVT-SMSAVEFTPLPT 303
Db 596 FIDGIRKQFGSSMLVN-SVKVAEFGRLATVHSSRLGRPPGSLTGSRLPLDFATVNE 654
QY 304 CLQHRSCDACMSDITFNCISWCH--VLQRCSSGFDYRQEWMDYCAQAEAE 352
Db 655 AVNVISCWYEDKTENGFNVGWYIGSVTDVYTGFRMHEKGWRSFYCVTEPD 705
RESULT 5
T09173
EH domain protein Repsl - mouse
N:Alternate names: RalBP1-associated EH domain protein Repsl
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09173
R:Yamaguchi, A.; Urano, T.; Goi, T.; Feig, L.A.
J. Biol. Chem. 272, 31230-31234, 1997
A:Title: An eps homology (EH) domain protein that binds to the ral-GTPase target, RalBP1
A:Reference number: Z16602; MUID:98058900; PMID:9395447
A:Accession: T09173
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-743 <YAM>
A:Cross-references: EMBL:AF031939; NID:q2677842; PIDN:AAB94736.1; PID:q2677843
A:Experimental source: cell line: C2C12; tissue type: muscle
C:Genetics:
A:Gene: repsl
C:Keywords: signal transduction

Query Match 3.8%; Score 101.5; DB 2; Length 743;
Best Local Similarity 18.3%; Pred. No. 4.9;
Matches 91; Conservative 63; Mismatches 166; Indels 177; Gaps 23;
QY 19 LSPQAGH-DEGPGSGMAK-----GTVGRNRRARESPGHV 55
Db 78 IPPPGRGVKGPGSHDAVQPPSAEQEPASPVVSPQSPPTSPHTWKHSRHPSGN 137
QY 56 SEPDRQLSQ-----DLGGGLAMDTLPDNRTRVVEDNHSYVYVSRLYGPSPHRELWV 109
Db 138 SERPLTGPFPWFSPFGDAQAGSAGDAV-----WSQSPPPPPQDNV 179
QY 110 DVAF-----ANRSQVKIHTILS-NTHQASRVLSFDPPYGHPLQITAT 155
Db 180 SFADTPTTSALLTMHPASVODQTVTVASATAANIRQSSYEDPW-----KITDB- 232
QY 156 GGFIFMGDVITHRLMTATQY--VAPLMANFNPGYSNDSTVYVYFDNGTVFVQWHDVY-LOG 212
Db 233 -----QRQYVYVQKTIQPDNLGTFP---SAAKEFTKSKLPILELSHIWELSD 279
QY 213 WEDKSGFT---FOALHHDGRIVFAYK---EIPMSVPEISSQHPVKTKGLSDAFMLNPS 266
Db 280 FDKDGLTLDDEFCAAFH---LVVARKNGYDLPEKLPE-----SLMPKLLIDLEDS 325

QY 267 PDVPESSRRSIFBYHRIELDPKSVKTSMSAVEFTPLTCLQHRSCDACMSDITFNCISWCH 326
Db 326 ADVGEQGEVGYSGSAEAPPSPSPSL-----NOTWPE 361
QY 327 VLQRCSSGFDYRQEWMDYCAQAEAGRMCEDEQFDEHDSASPDTS----- 372
Db 362 LNQS-----SEQWETFS-ERSSSQTLTQF-DSNIAPADPDTAIVHPVPIRMTPSKI 411
QY 373 -----PSPYDGLTITSSSLFIDSLTTEDDTKLP-----VAGDGLONNLS 414
Db 412 HMOEMELKRTSSDHTNTPSLLVKPDLSEENKINSVKRPPSGNTVDGYSSSDSFFSD-- 469
QY 415 PKTKGTPV-----HLGT 426
Db 470 PEQIGSSVTRQSRHSCT 486
RESULT 6
E86345
hypothetical protein F16F4.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: E86345
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-733 <SPO>
A:Cross-references: GB:AE005172; NID:g8920637; PIDN:AAF81359.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; p
Query Match 3.8%; Score 101; DB 2; Length 733;
Best Local Similarity 24.1%; Pred. No. 5.3;
Matches 59; Conservative 24; Mismatches 72; Indels 90; Gaps 13;
QY 257 SDAFMILNPSDPVPSRRRSI-----FEYHRIELDPKSVKTSMSAVE-FTPLPTCL 305
Db 139 STGCMSLCDTTPPPNSKNGVGCRCRTEVSIPLDSHRIETQPSRPFENTSVEHNP----- 193
QY 306 QHRSCD-ACMSDITFNC-----WCHVLRQ-----SS 333
Db 194 ----CSYAFFYEDGMENFSSLEDLKLNRNTRFPVLLDWSIGNOTCEQVYVGRNITCGNST 249
QY 334 GFDRYRQSWMDYCAQAEAGRM-----CEDFOD---EDHDSASPD-----SF---SPY 376
Db 250 CFDRTRGKYCKCLQGFDPGNPYLSDGQDLINECTTRIHCNSDTSTCENTLGSFHCQCP 309
QY 377 DGLTITSSSLFIDSLATEDDTKLNPNYAGSDGLONNLSPKTKG-TPVHLGTIVGIVLAVL 435
Db 310 GSDLNTTMSG-IDTPKEE-----PKYLGWTTVLLGTTIGTLILL 349
QY 436 LVAAT 440
Db 350 TISYI 354
RESULT 7
SI8606
phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Rhizobium sp.
C:Species: Rhizobium sp.
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Feb-2001

C:Accession: S18606
R:Osteras, M.; Finan, T.M.; Stanley, J.
Mol. Gen. Genet. 230, 257-269, 1991
A:Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, encoding
A:Reference number: S18606; MUID:92079905; PMID:1720862
A:Accession: S18606
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-535 <OST>
A:Cross-references: EMBL:X63291
C:Superfamily: phosphoenolpyruvate carboxykinase (ATP)
C:Keywords: carbon-carbon lyase; carboxy-lyase; nucleotide binding; P-loop
F:234-241/Region: nucleotide-binding motif A (P-loop)

Query Match 3.7%; Score 100; DB 2; Length 535;
Best Local Similarity 19.8%; Pred. No. 4.2;
Matches 71; Conservative 50; Mismatches 157; Indels 80; Gaps 15;

QY 11 VLREARALSPQAGHDEGSGWAAKGTVRGNRRRARESPGHV--SEDPRTQLSODLG 68
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
17 VFRPLGRSLQURAELEYEE---AFARGALTAHGCALTCGHTGRSPKDKYVVRDAAT 72
QY | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
69 GQTLAMDT---LPDNRTRVVED-----NHSYVSRLYGPSEPHSRRELWVDVAEANKSQ 118
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
73 GDOIWDDNNSAISPENPERLRQDMLAHAKGMSLYVDLVGAGQSGK-----CVADARRHR 127
QY | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
119 VKIHTI-LSNTHRQASRVLS-----FDPP-FYGHP-----LRQITIA 154
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
128 IRWHSFLTRNLIRPPREGSLAFPLKLTIIDLPFKAMPERHGRGRTIACDLTKGLVL 187
QY | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
155 TGGFTFMGDVTHRLMTATQYVAP-----LMANFPGYSNDSTVYVF----- 195
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
188 IGGTSYAGEMKSVFTVLYLLPNKAVMPHCSANVGA---GDTAIFGLSGTGKTTLS 244
QY | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
196 -DNGTVFVQNDHYVLOGWEDKGSFTQAALHHDGRIVFAYKEIPMSVPEISSQHPVK 254
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
245 ADPNRTLTGDDH---GWSDKGVNEFEG-----GCYAKAIRLSEAAEPEIFATRRFGT 295
QY | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
255 GLSDAFMILNPDVPESRRSIFEHRIELDPKVTSMASVETPTPTCLQHRSCDA 312
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
296 VVENVVDERRAPDFDNG---SLTENTRIAYPLDFIPNASETGTAPOPTIIMLTADA 350

RESULT 8
T12529
hypothetical protein DKFZp434P113.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: T12529
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17524
A:Accession: T12529
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1133 <WAM>
A:Cross-references: EMBL:AL080145
A:Experimental source: adult testis; clone DKFZp434P113
C:Genetics:
A:Note: DKFZp434P113.1

Query Match 3.7%; Score 99; DB 2; Length 1133;
Best Local Similarity 23.0%; Pred. No. 14;
Matches 67; Conservative 37; Mismatches 119; Indels 68; Gaps 16;

QY 162 GDVTHRLMTATQYVAPLMANFNPGYSNDSTVYFDNGTFVQWDHYVLOG--WE----- 214
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
823 GDIAH--IYDITQGNKLLTFNPDLANN---YKRCATENPTDDLVLNDGVLDVRSQA 876
QY | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
215 -----DKGSTFFQALHHDGRIVFAKEI-----PMSVPEISSQ---HPVKTGLSD 258
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
877 AIHKFDKFNMNISGVFHPNGLVLEIINTEIWDLRTFHLHTVPALDQCVRVFNHTGTVMYG 936

QY 259 AFMILNPDVPESRRSIFEHRIELDPKVTSMASVETPTPTC-LQHRSCDAMSSD 317
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
937 AMLQADDEDDLMERKSPF-----GSSFTFNATDYKPIATIDVARNFDLCTD-- 986
QY 318 LTFNCWCHVLQRCSSGFDYRQEWMDYGC-----AQEAEGMCEDFODEDH 364
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
987 -TKDC-YLAVIENQGS-MDALN--MDTVCRLYEVGRQLAEDEDEDEDEDEDEEDD 1040
QY 365 DSASPDTSFSPYDGLTTTSSSLFIDSLTTEDTKLNPNYAGGDLONNLSP 415
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
1041 DEDDDDTD-----DLDELDTQLLEALEEDDN--NENAGEDG-DNDFSP 1082

RESULT 9
T16074
hypothetical protein F14B8.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16074
R:Geisels, C.
submitted to The EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F14B8.
A:Reference number: Z18456
A:Accession: T16074
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-345 <CEI>
A:Cross-references: EMBL:U28737; NID:g860717; PID:g860723; PIDN:AAA68276.1; CBSP:F14B
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CBSP:F14B8.6
A:Introns: 17/3; 61/2; 93/3; 144/2; 197/1; 218/3; 255/2; 327/3

Query Match 3.6%; Score 98; DB 2; Length 345;
Best Local Similarity 18.7%; Pred. No. 3.3;
Matches 50; Conservative 46; Mismatches 95; Indels 76; Gaps 12;

QY 240 MSVPETSSSQHPVKGLSDAFMILNPDVPESRRSIFEHRIELDPKVTSMASVET 299
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
96 ISVSGIATKCATLGNASDSFLMTQSSNQPNRNNQ-----TPIQVTS-NTNQWT 145
QY 300 PLPTCLQHRSCDAMSSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGMCEDF 359
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
146 LTATI--NRKCG--ADQYGFNCN-----EQCT-----VNNDYYCYTCGSGNKTCAS- 191
QY 360 QDEHDHSDSPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPNYAGGDLONNLSPKTKG 419
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
192 -----GDVNPD-DCSYVDHPISTTWS-----NTQCSASAE 222
QY 420 TPVHLGTIVGIVLAVLLVAAIL-----AGIV-----INGHTSNAALFF 459
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
223 TYFWLMISFAIIIAIILAILLLVLELCCGLFTGRQSARRSDEGDWIVPKTPKANHELYD 282
QY 460 IERRPHHPAMKFRSHPDHSTYAEVEP 486
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
283 ADITPHH---QYRRHRQDNNNGESTEP 306

RESULT 10
S45429
probable membrane protein YBL079w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YBL0725
C:Species: Saccharomyces cerevisiae
C:Date: 09-Jun-1994 #sequence_revision 09-Sep-1994 #text_change 21-Jul-2000
C:Accession: S45429; S45820; S45815; S59226
R:Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
submitted to the EMBL Data Library, May 1994
A:Description: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces
A:Reference number: S45429
A:Accession: S45429
A:Molecule type: DNA
A:Residues: 1-1502 <OBE>
A:Cross-references: EMBL:X79489; NID:g496661; PID:g496702

A: Experimental source: strain S288C
 R: Domdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.
 submitted to the Protein Sequence Database, August 1994
 A: Reference number: S45816

A: Accession: S45820
 A: Molecule type: DNA

A: Residues: 1-1502 <DOM>

A: Cross-references: EMBL:Z35840; NID:G536126; PID:G536127; MIPS:YBL079w

A: Experimental source: strain S288C
 R: Contreras, R.; Fiers, W.; Logghe, M.; Molemans, F.
 submitted to the Protein Sequence Database, August 1994
 A: Reference number: S45802

A: Accession: S45815

A: Molecule type: DNA

A: Residues: 1262-1502 <CON>

A: Cross-references: EMBL:Z35840; MIPS:YBL079w

A: Experimental source: strain S288C
 R: Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
 Yeast 11, 1103-1112, 1995

A: Title: Sequence analysis of a 78.6 kb segment of the left end of *Saccharomyces cerevisiae*
 A: Reference number: S59184; MUID: 96076635; PMID: 7502586

A: Accession: S59226

A: Status: nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-1502 <OBW>

A: Cross-references: EMBL: X79489; NID: G496661; PID: G496702

A: Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994

C: Genetics:

A: Gene: SGD: NUP170

A: Cross-references: SGD: S0000175; MIPS: YBL079w

A: Map position: 2L

C: Keywords: nucleus; transmembrane protein

F: 231-247/Domain: transmembrane #status predicted <TM1>

F: 434-450/Domain: transmembrane #status predicted <TM2>

F: 764-780/Domain: transmembrane #status predicted <TM3>

F: 1311-1327/Domain: transmembrane #status predicted <TM4>

F: 1382-1399/Domain: transmembrane #status predicted <TM5>

F: 1406-1423/Domain: transmembrane #status predicted <TM6>

Query Match 3.6%; Score 98; DB 2; Length 1502;

Best Local Similarity 22.7%; Pred. No. 25;

Matches 62; Conservative 41; Mismatches 106; Indels 64; Gaps 14;

QY 61 TOLSDLGCGTGLMTDPLDNRVYEDNHSYVSRLYGCPSPHRSRLWVDVAEANRQVK 120

DB 778 TLLRLDINGRHVFM-TFTDNV---TSHAFISS--DPTTPSINNLSKSEISQNRNLI- 829

QY 121 IHTLSNTHRQASRVVLSFD-FPYGHPRLQITATGGFIPMGDVIHRLMTATQYVAP-L 178

DB 830 -----SKVISKDCIEYV---LSSINILNEFFITYGDSI-----SOISAPYV 868

QY 179 MANFNPGYSDNSTVYFD-----NGTVFVQWDHVVYVQWEDKSGFTFOALHHDGRI 231

DB 869 LANNNGRVIDKTEEVANQASIAINAMIKWQ-----SIKGLSFLNVLVESEV 919

QY 232 -----VFAYKEIPMSVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRRRIFEYHRIEL 285

DB 920 EGFNDNQYLGFKDI-ISFVSLDVQKDLVLKDFKDLF-----APNDKTKSLIREILLSI 970

QY 286 DPKSVTMSAVEFTPLPTCLQHRSCDACMSDDL 318

DB 971 INRNITKGASIEY--ATATQERCSCGSCASDI 1001

RESULT 11

I83196

NEDD-4 ORF - mouse (fragment)

C: Species: Mus musculus (house mouse)

C: Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000

C: Accession: I83196

R: Kumari, S.; Tomooka, Y.; Noda, M.

Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992

A: Title: Identification of a set of genes with developmentally down-regulated expression

A: Reference number: I60167; MUID: 92328780; PMID: 1378265

A: Accession: I83196

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-708 <RES>

A: Cross-references: GB: D10714; NID: G220508; PID: G220509

C: Genetics:

A: Gene: NEDD-4

C: Superfamily: rat ubiquitin-protein ligase; protein kinase C 2 region homology; ubi

F: 40-77/Domain: WW repeat homology <WW1>

F: 196-233/Domain: WW repeat homology <WW2>

F: 251-288/Domain: WW repeat homology <WW3>

F: 347-682/Domain: ubiquitin-protein ligase homology <UB1>

Query Match 3.6%; Score 97; DB 2; Length 708;

Best Local Similarity 19.4%; Pred. No. 11;

Matches 94; Conservative 51; Mismatches 154; Indels 186; Gaps 25;

QY 14 EAARALSP-----QPGAG---HDEGPG---SGWAAKGTVRG---WNRRARESPGHVS 56

DB 12 DQAELEPGWVLDQDPAATHLPHPPEPSPPLPGWEERQDVLGRTYYVNHESRRQTQWRP 71

QY 57 EPD-----RTQLSDLGCGTGLMTDPLDNR-RRSIFEVHRIELDPSKV 290

DB 72 SPDDDLTDEDNDMDQLQAORAFTRRQISSEVDG-----PDNRESPENWEIVREDEN 123

QY 90 SYIVSR-LYGPSEPHSRRLWVDVAEANRQVKIHTLSNTHRQASRVVLSFDF----PFY 144

DB 124 TEYSQAVQSPPSGH-----IDV-----QTH-----LAEFENTRLAVC 156

QY 145 GHPLRQITATGGFIPMGDVIHRLMTATQYVAPLM-----ANFNPGY-----SONSTVYVFD 196

DB 157 GNPATSQPVTSSNHSRSGSLQTCIFEQPTLPVLLPTSGPLPGWEEKQDGRSYYVD 216

QY 197 NGTVFVQWDHVVYQ-----GWEDKSGFTFOALHHDGRI 231

DB 217 HNSK-TTTSKPTMQDDPRSKIPALHRGKTDSNDLGLPLPGWBER-----THTDGRV 267

QY 232 VFAYKEIPMSVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRSIFEVHRIELDPSKV 290

DB 268 FFNNHNIKTQWEDPRLQNVAITG-----PAPVYSRDYKRYKKEFFRKLKKQ-- 314

QY 291 TMSAVEFTPLPTCLQHRSCDACMSDDLTFNCSWCHVLQRCSSGDPDRYQEWMDYCAOE 350

DB 315 -----TDIPNKEFMK-----LRRANILEDYSYR-IMGVKKRADL 346

QY 351 AEGRMCEFDQDE---DHDSASPD-----TSFSPYDGLTFTSSSLFIDSLTDEDTKL 400

DB 347 LKARLWIEFDGKLDYGGVAREWFFLISKEMFNPIYG-----LFEYSATDNTYLOI 398

QY 401 NPYAG 405

DB 399 NPNSG 403

RESULT 12

S33415

corticosteroid-binding globulin precursor - mouse

C: Species: Mus musculus (house mouse)

C: Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 16-Jul-1999

C: Accession: S33415; S43740

R: Scroccchi, L.A.; Orava, M.; Smith, C.L.; Han, V.K.M.; Hammond, G.L.

Endocrinology 132, 903-909, 1993

A: Title: Spatial and temporal distribution of corticosteroid-binding globulin and its

A: Reference number: S33415; MUID: 93145908; PMID: 7916682

A: Accession: S33415

A: Molecule type: mRNA

A: Residues: 1-397 <SCRI>

A: Cross-references: EMBL: X70533; NID: G298114; PID: CAA4934.1; PID: G298115

A: Accession: S43740

A: Molecule type: protein

A: Residues: 23-40 <SCR2>

C: Superfamily: antithrombin III

C:Keywords: glycoprotein; steroid binding
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-397/Product: corticosteroid-binding globulin #status experimental <MAT>
F:89,169,217,232,253,320/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.6%; Score 96.5; DB 2; Length 397;
Best Local Similarity 20.2%; Pred. No. 5.3;
Matches 53; Conservative 47; Mismatches 104; Indels 59; Gaps 11;

QY 61 TQLSODLGGGTLMADTLPDNRTRVVDNHSYVSKLYGSPSEPHSRELWVDVAE-----A 114
DB 114 TGLENNMWNVFLQNLKLSFLADPKHYEALIPSKD-----WTAGQGINNHVK 168
QY 115 NRSQVKIHTLSNTHROASRVVLSDFE-----PFYGHPLRQTTIATGCFIFMGDVIHR 167
DB 169 NKTQKIEHVYVSDLDSSATLILINIELKGIWKLFPSPENTRE-----EDFYV 216
QY 168 MLTATQVYAPLMAFNFCYSDNSVTV-----YFDNGTVFVQWDHVIYQWEDKGSFT 220
DB 217 NETSTVKPMVQSGNISYFRDPAICQMVMQNVGNGTTFIILPD-----QGQMD-----T 268
QY 221 FQAALHHD-----GRIVFAYKEIPMSPEISSQH-----PVKTGLSDAFMILNPSDV 269
DB 269 VVAALNRDTIDRWGKLMIP-RQMNLYIPKFSMSDYDLQDLADVGKIDLFNQSDFADT 327
QY 270 PESRRRSIFEYHR--IELDPSKV 290
DB 328 TKDTPLTTLTLHLKAMQLQDEGNV 350

RESULT 13

T19703

hypothetical protein C34C12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19703

R:Kershaw, J.

submitted to the EMBL Data Library, December 1994

A:Reference number: Z19166

A:Accession: T19703

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-679 <WIL>

A:Cross-references: EMBL:Z46996; PIDN:CAA87102.1; GSPDB:GN00021; CESP:C34C12.2

A:Experimental source: clone C34C12

C:Genetics:

A:Gene: CESP:C34C12.2

A:Map position: 3

A:Introns: 5/3; 72/3; 125/3; 173/3; 511/3; 605/3

Query Match 3.6%; Score 96.5; DB 2; Length 679;
Best Local Similarity 23.3%; Pred. No. 11;
Matches 70; Conservative 36; Mismatches 130; Indels 65; Gaps 12;

QY 16 ARALSPQAGHDEGGGCGWAAAGTVRGWNRRAESPGHVSEPDRTQLSODLGGGTAMD 75
DB 337 AKYLKPDQPTSSACGKPYFESTSSSRKPTASPG---PPGRTQISDQLNTGEVRY- 392
QY 76 TLPDNRTRVVDNHSYVSKLYGSPSEPHSRELWVDVAEANRSQ---VKIHTILSNTHROA 132
DB 393 -----VNSGKPFNF-----SESNRNLKIPGIYKRPFRYIKPEGFTSASYKQAQ 439
QY 133 SRVLSDFDFYGHPLRQITAT-----GGFTFMGDVTHRMCTATQYVAPLMAFNPNQY 186
DB 440 SEGMSF-----LKTGSATPENSCKSAHDFMDI-----SSTPYKSHVVVSEDMN 486
QY 187 SDNSTVYVF-----DNGTVFVQWDHVIYQWEDKGSFTFOAALHHDGRIVFAYKEIPMS 241
DB 487 SSSTTGGFSEKDKGAL-----GSQKSPMPDIATALHN-----IFDSKEVQSS 531
QY 242 VPEISSSQHVKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVKTSMAVEFTPL 301
DB 532 SSTTGSAPPENSKSDHF-----DMPDISSTLYRSRVE---PISSSSSSGTSTISAPRYVPK 585

QY 302 P 302
DB 586 P 586

RESULT 14

S71480

homeotic protein Hox B3 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S71480

R:Scotting, P.J.; Rex, M.

submitted to the EMBL Data Library, August 1993

A:Reference number: S71480

A:Accession: S71480

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-399 <SCO>

A:Cross-references: EMBL:X74506; NID:G398704; PIDN:CAA52613.1; PID:G443794

C:Genetics:

A:Gene: Hox-B3

C:Superfamily: homeotic protein Hox B3; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:160-216/Domain: homeobox homology <HOX>

Query Match 3.5%; Score 95.5; DB 1; Length 399;
Best Local Similarity 20.5%; Pred. No. 6.5;
Matches 62; Conservative 40; Mismatches 110; Indels 91; Gaps 10;

QY 246 SSSQHPVKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKSVTMS-----AVEFT 299
DB 94 STSSNISPGSAKVPKPTSVQTP-SLTQKIFPMKESRQNSKOKSSPSTETCSGEKT 152
QY 300 PLPTCLQHRSCDACWSSDLT-----ENCWCH-----VLQRCSSGFDRYQEW-----M 343
DB 153 PGSSASRRARTAYTSAQLVELEKEFHFNLCRPRRVEAMNLLNLSERQIKMFQNRMM 212
QY 344 DYGCAQAEGRMCEDFQDEHDHDSASPDTSFSP-----VDGLTFTTSSSLFIDSLLT 394
DB 213 KYKDKQSKGM-----GSSSGGSPSTGPPQPMQSSAGFMALHTMSSNYDAPSPS 264
QY 395 EDTKLNIPYAGDGLQNNL-----SPKTKGTPTVHLGT 426
DB 265 LNKPHONAYHTVNTQNPDKGALQOKYNTAPEYDPHVLOGNVAYGTPSMQSGPVVYG- 323
QY 427 IVGIVLAVLLAAIILAGIYINGHPTSNAALEFFIERRPHHPAMKFRSHPDHSYAEVEP 486
DB 324 -----GNVDSLPTSGPSLYGLNHLPHHQA-----NMDYSGPPQMP 361
QY 487 SGH 489
DB 362 SQH 364

RESULT 15

S70642

ubiquitin ligase Nedd4 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000

C:Accession: S70642

R:Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.

EMBO J. 15, 2371-2380, 1996

A:Title: WW domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na(

A:Reference number: S70642; MUID:96221297; PMID:8665844

A:Accession: S70642

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-887 <STA>

A:Cross-references: EMBL:U50842; NID:G1293646; PIDN:AA848949.i; PID:G1293647

C:Genetics:

A:Gene: Nedd4

C:Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubi

F:54-167/Domain: protein kinase C C2 region homology <KC2>
F:246-283/Domain: WW repeat homology <WW1>
F:402-439/Domain: WW repeat homology <WW2>
F:459-496/Domain: WW repeat homology <WW3>
F:555-881/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 3.5%; Score 95.5; DB 2; Length 887;
Best Local Similarity 19.2%; Pred. No. 20;
Matches 93; Conservative 55; Mismatches 155; Indels 181; Gaps 25;

QY	14	EAARALSP-----QPGAG-----HDEGPG-----SCWAAKGTVRG-----WNR	47
Db	218	DOAELEPGVWVLDQPDAAHLQHPPEPLPPGWEERQDVLGRYYVNVNHSRTQWKR	277
QY	48	ARES-----PGHVSEPORTQLSODLGGTGLAMDLPDNRTR-----VVEDNH	89
Db	278	SPEDDLTDENGDIQLQAHGAFTRRQJSEVDVG-----PDNHESPENWEIVREDEN	329
QY	90	SYVSR-LYGPSEPHSRELWVDAEANKRSQVKIHTILSNTHRQASRVVLSDFPFYGHPL	148
Db	330	TIYSQAVQSPSGHP-DVQVRLAE-----ELDTRLT-----MYGNPA	366
QY	149	ROITATGGFTFMGDVIRHMLTATQYVAPLM-----ANENPGY-----SDNSTVYFDNGTV	200
Db	367	TSQPVYSSNHSRGGSSQTCIFEQPTLPVLLPTSSGLPPGWEERQDDGRGRSYVDHNSK	426
QY	201	FVQWDHVYVLO-----GWEDKGSFTFQAALHHDGRIVF	233
Db	427	TTWSKPTMQDDPRSKIPAHLRGKTPVDSNDLGLPLPGWEER-----THTDGRVFF	477
QY	234	AYKEIPMSVPEISSQHPVKTGLSDAFMLNPSDPVPESR-RRSIFEYHRIELDPKSVTS	292
Db	478	INHNKKTQWEDPRMQNVAITG-----PAEPYSRDYKRKYEFRRKLKKQ-----	522
QY	293	MSAVEFTPLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRIYQREWMDYCAQAE	352
Db	523	TDIPNKFEMK-----LRRANILEDYSYRR-IMGVRRADFLK	556
QY	353	GRMCEDFODE---DHDSASPD-----TSFSPYDGLTTTSSSLFIDSLTDEDT-KLN	401
Db	557	ARLWIEFDGCKLDYGGVAREWFFLLISKEMFNPIYG-----LFEYSATEDNWTLOIN	608
QY	402	PYAG	405
Db	609	PNSG	612

Search completed: April 22, 2003, 16:08:19
Job time : 26 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:14:56 ; Search time 45 Seconds

(without alignments)
1068.160 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 500

Sequence: 1 MRCLEWLLVLRARALS.....YAEVPSGHEKGFMEAEQC 500

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR.73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	1.8	655	E69791	conserved hypotet
2	8	1.6	224	T36146	hypothetical prote
3	8	1.6	317	T30232	methyitransferase
4	8	1.6	363	E84280	hypothetical prote
5	8	1.6	429	C41903	arsenical pump mem
6	8	1.6	472	E81817	probable sodium/al
7	8	1.6	472	F81058	amino acid symport
8	8	1.6	476	T19786	hypothetical prote
9	8	1.6	483	T35715	export protein - S
10	8	1.6	562	A12507	hypothetical prote
11	8	1.6	751	T46517	hypothetical prote
12	7	1.4	75	W5WL33	E5 protein - human
13	7	1.4	76	W5WL58	E5 protein - human
14	7	1.4	78	S08449	hypothetical prote
15	7	1.4	82	G97758	hypothetical prote
16	7	1.4	100	A43998	hypothetical prote
17	7	1.4	106	QJ1248	hypothetical 12K p
18	7	1.4	114	T08325	hypothetical prote
19	7	1.4	131	T01293	hypothetical prote
20	7	1.4	133	A97192	hypothetical prote
21	7	1.4	147	AD0539	hypothetical prote
22	7	1.4	150	F87589	hypothetical prote
23	7	1.4	154	AD3475	protein-Npi-phosph
24	7	1.4	166	F97128	probable membrane
25	7	1.4	170	F87482	hypothetical prote
26	7	1.4	177	F87600	conserved hypotet
27	7	1.4	178	E75340	conserved hypotet
28	7	1.4	186	F97395	modulation protein
29	7	1.4	186	AH2613	modulation protein

hypothetical prote
capsular polysacch
conserved hypotet
E1 membrane glycop
E1 membrane glycop
E1 membrane glycop
E1 membrane glycop
hypothetical prote
probable integral
probable transcrip
conserved hypotet
probable membrane
hypothetical 30.5K
moac protein [mpo
probable [imported
F24J8.7 protein -
probable transport
iron(III) dicitrat
hypothetical prote
cytochrome c-type
hypothetical secre
hypothetical prote
transcription regu
ribose transport s
LacI-family trans
probable ABC trans
probable integral
probable carboxyno
invasion protein i
cell invasion prot
probable cytochrom
cell division prot
probable rod shape
hypothetical prote
protein secretion
imidazoloneproton
conserved hypotet
sodium/glutamate s
heat shock protein
heat shock protein
heat shock protein
colligin-2 - human
hypothetical prote
Spa47 protein - Sh
uracil permease Ur
probable GDP-4-ket
diacylglycerol o-a
probable secretion
hypothetical prote
hypothetical prote
hypothetical prote
probable type II s
dihydropolipamide d
microsome-associat
probable imidazolo
cannabinoid recept
hypothetical prote
L-xylokinase (EC
L-xylokinase (EC
conserved hypotet
probable integral
diacylglycerol O-a
hypothetical prote
hypothetical prote
acetyl-CoA/acetox
probable chemotaxi
Na+ ATPase chain J
NAD-diphthamide AD
NAD-diphthamide AD
probable ATP-bindi
cytochrome-c oxida
heat shock protein
dnak-type molecula
hypothetical prote

103	7	1.4	622	2	S57684	protable membrane	176	6	1.2	100	1	S27016	defensin alpha-6 p
104	7	1.4	627	2	A99607	hypothetical prote	177	6	1.2	100	2	B28487	apolipoprotein C-I
105	7	1.4	630	2	T31017	hypothetical prote	178	6	1.2	100	2	G87478	hypothetical prote
106	7	1.4	643	2	E82481	methyl-accepting c	179	6	1.2	102	2	F69475	conserved hypotet
107	7	1.4	660	1	A54942	acyl-CoA oxidase (180	6	1.2	102	2	S50936	hypothetical prote
108	7	1.4	660	1	B54942	acyl-CoA oxidase (181	6	1.2	104	2	B82294	probable membrane
109	7	1.4	660	2	I38095	hypothetical prote	182	6	1.2	104	2	A23301	hypothetical prote
110	7	1.4	662	2	T17211	NADPH-ferrihemopro	183	6	1.2	105	2	A23301	hypothetical prote
111	7	1.4	693	1	S38427	probable DNA-direc	184	6	1.2	108	2	J01428	hypothetical 11.6K
112	7	1.4	704	2	T03478	histidine ammonia-	185	6	1.2	109	2	B98066	conserved hypotet
113	7	1.4	723	2	AG3555	cytoskeletal prote	186	6	1.2	109	2	T29123	hypothetical prote
114	7	1.4	751	2	T01449	hypothetical prote	187	6	1.2	110	2	B69227	hypothetical prote
115	7	1.4	763	2	F96693	glycosyltransferas	188	6	1.2	110	2	D72673	hypothetical prote
116	7	1.4	769	2	E97092	protein containing	189	6	1.2	110	2	A82194	hypothetical prote
117	7	1.4	773	2	E97071	cadherin 12 - huma	190	6	1.2	110	2	A33934	sporozoite surface
118	7	1.4	794	2	I59372	transporter homolo	191	6	1.2	111	2	S27005	dnak-type molecula
119	7	1.4	885	2	B69783	hypothetical prote	192	6	1.2	111	2	A58866	hypothetical prote
120	7	1.4	891	2	A97718	methyl-accepting c	193	6	1.2	111	2	AE0794	probable membrane
121	7	1.4	953	2	S75285	probable zinc-bind	194	6	1.2	114	2	B34792	ig heavy chain pre
122	7	1.4	999	2	T36021	Na+/Ca2+,K+-exchan	195	6	1.2	115	2	G87300	dihydroneopterin a
123	7	1.4	1014	2	T31433	hypothetical prote	196	6	1.2	116	2	H90966	hypothetical prote
124	7	1.4	1065	2	A70797	hypothetical prote	197	6	1.2	117	2	T07864	germination-specif
125	7	1.4	1092	2	S42798	fibronectin-bindin	198	6	1.2	118	2	S45680	lipid transfer pro
126	7	1.4	1096	2	C87263	hypothetical prote	199	6	1.2	118	2	C84806	probable nonspecif
127	7	1.4	1120	2	S46111	probable membrane	200	6	1.2	119	2	C81821	probable integral
128	7	1.4	1172	2	S32689	paraspinal crystal	201	6	1.2	120	2	C91027	D-erythro-7,8-dihy
129	7	1.4	1184	2	T09484	cartilage intermed	202	6	1.2	120	2	D85871	D-erythro-7,8-dihy
130	7	1.4	1199	2	S20969	Na+/Ca2+,K+-exchan	203	6	1.2	120	2	E65002	D-erythro-7,8-dihy
131	7	1.4	1245	2	T42920	hypothetical prote	204	6	1.2	120	2	T17514	hypothetical prote
132	7	1.4	1308	2	B75198	DNA helicase relat	205	6	1.2	121	2	B87648	hypothetical prote
133	7	1.4	1628	2	F86194	hypothetical prote	206	6	1.2	122	2	T01589	acyl carrier prote
134	7	1.4	2126	2	H70821	probable polyketid	207	6	1.2	122	2	B70764	hypothetical prote
135	7	1.4	2391	2	T18410	carbamoyl-phosphat	208	6	1.2	124	1	FPMV4	vicilin, 14K compo
136	7	1.4	3670	2	T36249	CDA peptide synthet	209	6	1.2	124	2	H69520	conserved hypotet
137	7	1.4	3944	2	T19997	hypothetical prote	210	6	1.2	124	2	S76185	hypothetical prote
138	6	1.2	11	2	A61483	pyridoxal kinase (211	6	1.2	124	2	B84258	hypothetical prote
139	6	1.2	43	2	S32641	cytochrome-b5 redu	212	6	1.2	124	2	H89794	hypothetical prote
140	6	1.2	47	1	D32535	colicin E5 lysis p	213	6	1.2	126	2	I36914	CB59 protein - bab
141	6	1.2	47	1	JQ0330	colicin E5 lysis p	214	6	1.2	126	2	T02351	probable acyl carr
142	6	1.2	47	1	S27395	colicin E7 lysis p	215	6	1.2	126	2	S75413	hypothetical prote
143	6	1.2	47	1	S49178	colicin E4 lysis p	216	6	1.2	126	2	F87381	hypothetical prote
144	6	1.2	48	2	D89788	hypothetical prote	217	6	1.2	126	2	T31972	hypothetical prote
145	6	1.2	55	2	B82375	hypothetical prote	218	6	1.2	127	2	B64034	hypothetical prote
146	6	1.2	66	2	S03443	dnak-type molecula	219	6	1.2	127	2	G82038	conserved hypotet
147	6	1.2	68	2	S68975	tetrahydromethanop	220	6	1.2	128	1	S12372	spasmolytic protei
148	6	1.2	68	2	C69021	ig heavy chain V-A	221	6	1.2	128	2	I36894	CB59 protein - gre
149	6	1.2	70	2	A30518	hypothetical prote	222	6	1.2	130	2	T29155	hypothetical prote
150	6	1.2	71	2	F69981	hypothetical prote	223	6	1.2	131	2	H82337	preprotein translo
151	6	1.2	74	2	AH1892	hypothetical prote	224	6	1.2	131	2	T02500	hypothetical prote
152	6	1.2	76	2	T36658	hypothetical prote	225	6	1.2	131	2	F71148	hypothetical prote
153	6	1.2	78	2	T17494	sopC protein - Esc	226	6	1.2	132	2	I47191	ig heavy chain var
154	6	1.2	79	1	BVECCF	hypothetical prote	227	6	1.2	132	2	T08676	hypothetical prote
155	6	1.2	80	2	E82500	antigen 7H8/1 - ma	228	6	1.2	134	2	B82768	virulence regulato
156	6	1.2	81	2	B60396	hypothetical prote	229	6	1.2	134	2	A86475	15.8K F12A4.7 hypo
157	6	1.2	85	2	G86426	hypothetical prote	230	6	1.2	135	2	PN0527	G protein-coupled
158	6	1.2	88	2	A84342	hypothetical prote	231	6	1.2	135	2	T35853	probable oxidoredu
159	6	1.2	88	2	AG1356	ribosomal prote	232	6	1.2	135	2	F75137	hypothetical prote
160	6	1.2	89	2	E82919	sugar transport pr	233	6	1.2	137	2	S52360	superoxide dismuta
161	6	1.2	89	2	A81013	hypothetical prote	234	6	1.2	137	2	S52362	superoxide dismuta
162	6	1.2	89	2	F82757	hypothetical prote	235	6	1.2	137	2	S52365	superoxide dismuta
163	6	1.2	91	2	F69069	conserved hypotet	236	6	1.2	137	2	S52376	superoxide dismuta
164	6	1.2	93	2	C90192	probable 60S ribos	237	6	1.2	138	2	H83013	conserved hypotet
165	6	1.2	93	2	H86472	hypothetical cytos	238	6	1.2	139	1	RKMLS	ribulose-bisphosph
166	6	1.2	94	2	AC3342	translation releas	239	6	1.2	139	2	H64064	tolR protein - Hae
167	6	1.2	96	2	A93377	hypothetical prote	240	6	1.2	139	2	H83663	hypothetical prote
168	6	1.2	96	2	AC1623	hypothetical prote	241	6	1.2	139	2	S38256	mannose-binding le
169	6	1.2	98	2	A11260	hypothetical prote	242	6	1.2	139	2	D86417	probable auxin-ind
170	6	1.2	98	2	S41562	hypothetical prote	243	6	1.2	140	2	S54227	ig mu heavy chain
171	6	1.2	99	2	H75494	hypothetical prote	244	6	1.2	141	2	I47178	ig heavy chain var
172	6	1.2	99	1	S25566	apolipoprotein C-I	245	6	1.2	141	2	H72540	hypothetical prote
173	6	1.2	99	2	S75918	probable ferredoxi	246	6	1.2	143	2	T20464	hypothetical prote
174	6	1.2	99	2	G97228	glu-TRNAGln amidot	247	6	1.2	144	2	T03563	probable ribosomal
175	6	1.2	99	2	B97837	(p)ppGpp 3-pyropho	248	6	1.2	144	2	C83633	hypothetical prote

249	6	1.2	145	2	S74292	hypothetical prote	322	6	1.2	162	2	T13574	NADH2 dehydrogenas
250	6	1.2	145	2	E84461	hypothetical prote	323	6	1.2	162	2	S75277	hypothetical prote
251	6	1.2	146	1	PSGA	phospholipase A2 (324	6	1.2	163	2	G75424	bacterioferritin c
252	6	1.2	146	2	T25640	hypothetical prote	325	6	1.2	164	2	S48319	probable membrane
253	6	1.2	147	1	LZQJE	lysosomal (EC 3.2.1	326	6	1.2	165	2	G48232	cysteine-rich exte
254	6	1.2	147	2	H86851	hypothetical prote	327	6	1.2	165	2	G84508	hypothetical prote
255	6	1.2	147	2	B86699	hypothetical prote	328	6	1.2	166	2	F96786	protein F10A5.11 (
256	6	1.2	148	1	PSHU	phospholipase A2 (329	6	1.2	166	2	B72626	hypothetical prote
257	6	1.2	148	2	B72782	hypothetical prote	330	6	1.2	167	2	S20066	parietal-type ri
258	6	1.2	148	2	T14784	hypothetical prote	331	6	1.2	167	2	H64444	hypothetical prote
259	6	1.2	149	2	F65169	ol149 protein - Esc	332	6	1.2	167	2	H83432	regulatory protein
260	6	1.2	149	2	B91206	hypothetical prote	333	6	1.2	168	2	S21041	cytochrome-c oxida
261	6	1.2	149	2	D86052	hypothetical prote	334	6	1.2	168	2	G71316	probable rod shape
262	6	1.2	149	2	E87344	ribonuclease p pro	335	6	1.2	168	2	B95330	hypothetical prote
263	6	1.2	149	2	F72677	hypothetical prote	336	6	1.2	170	2	F85093	hypothetical prote
264	6	1.2	150	1	NRBO	pancreatic ribonuc	337	6	1.2	172	2	B75338	thermoresistant gl
265	6	1.2	150	1	NRBOS	seminal ribonuclea	338	6	1.2	172	2	C69267	hypothetical prote
266	6	1.2	150	2	S43955	probable NADH2 deh	339	6	1.2	174	2	S01189	NADH2 dehydrogenas
267	6	1.2	150	2	S69530	hypothetical prote	340	6	1.2	175	2	B84828	hypothetical prote
268	6	1.2	151	2	A86695	hypothetical prote	341	6	1.2	176	2	B72004	shikimate kinase C
269	6	1.2	151	2	A12685	hypothetical prote	342	6	1.2	176	2	C86620	shikimate kinase I
270	6	1.2	151	2	AH1839	two-component syst	343	6	1.2	176	2	B81208	conserved hypotet
271	6	1.2	152	1	NRRT	pancreatic ribonuc	344	6	1.2	176	2	H75332	ankyrin-related pr
272	6	1.2	153	2	S15330	pancreatic ribonuc	345	6	1.2	177	2	A99606	hypothetical prote
273	6	1.2	153	2	S17837	sorbin - pig	346	6	1.2	177	2	T34292	FMRFamide-like pep
274	6	1.2	153	2	T09188	probable outer mem	347	6	1.2	178	2	A71512	hypothetical prote
275	6	1.2	154	2	F82633	probable protein d	348	6	1.2	178	2	C87677	hypothetical prote
276	6	1.2	156	2	A1036	probable lysozyme	349	6	1.2	179	2	S59503	ferric pseudobacti
277	6	1.2	156	2	A70968	hypothetical prote	350	6	1.2	180	2	AE1596	signal peptidase I
278	6	1.2	156	2	H72621	hypothetical prote	351	6	1.2	182	2	A02946	keratin, 59K type
279	6	1.2	157	2	A10927	probable lysozyme	352	6	1.2	182	2	S03259	methyl coenzyme M
280	6	1.2	157	2	D31327	IgE receptor alpha	353	6	1.2	182	2	T36728	probable DNA-bindi
281	6	1.2	157	2	S58014	probable olfactory	354	6	1.2	182	2	H82981	hypothetical prote
282	6	1.2	158	2	S37355	glutamate-ammonia	355	6	1.2	184	2	D87605	transcription regu
283	6	1.2	158	2	S91553	v-type sodium ATP	356	6	1.2	185	2	S73114	photosystem I chal
284	6	1.2	158	2	B69124	hypothetical prote	357	6	1.2	185	2	T07700	hypothetical prote
285	6	1.2	158	2	T14078	hypothetical prote	358	6	1.2	185	2	T49660	glucan 1,4-alpha-g
286	6	1.2	158	2	C86937	probable membrane	359	6	1.2	185	2	B97933	conserved hypotet
287	6	1.2	159	2	S40727	hypothetical prote	360	6	1.2	186	2	C72782	hypothetical prote
288	6	1.2	160	2	T17048	NADH2 dehydrogenas	361	6	1.2	189	1	G69355	hypothetical prote
289	6	1.2	160	2	C89832	hypothetical prote	362	6	1.2	189	1	E69040	probable 3-isoprop
290	6	1.2	160	2	A82214	hypothetical prote	363	6	1.2	189	2	A71569	hypothetical prote
291	6	1.2	161	2	A45000	peptidylprolyl iso	364	6	1.2	190	1	KLSSAA	calcium-binding pr
292	6	1.2	161	2	E48232	cysteine-rich exte	365	6	1.2	190	2	T10968	hypothetical prote
293	6	1.2	161	2	D81940	probable membrane	366	6	1.2	190	2	B83690	hypothetical prote
294	6	1.2	161	2	E81166	hypothetical prote	367	6	1.2	191	2	G87253	hypothetical prote
295	6	1.2	161	2	F69338	hypothetical prote	368	6	1.2	192	1	KLSSAB	calcium-binding pr
296	6	1.2	162	1	CFMWA	C-phycocyanin alph	369	6	1.2	192	2	T41413	thioredoxin peroxi
297	6	1.2	162	2	T10745	NADH2 dehydrogenas	370	6	1.2	192	2	C71543	probable phenylacr
298	6	1.2	162	2	T17047	NADH2 dehydrogenas	371	6	1.2	192	2	T37657	hypothetical prote
299	6	1.2	162	2	T17045	NADH2 dehydrogenas	372	6	1.2	192	2	A84727	hypothetical prote
300	6	1.2	162	2	T13487	NADH2 dehydrogenas	373	6	1.2	192	2	F71169	hypothetical prote
301	6	1.2	162	2	T14256	NADH2 dehydrogenas	374	6	1.2	193	2	AE1561	weakly molybdopter
302	6	1.2	162	2	T17036	NADH2 dehydrogenas	375	6	1.2	193	2	AF1204	molybdopterin-guan
303	6	1.2	162	2	T14247	NADH2 dehydrogenas	376	6	1.2	194	2	C82041	general secretion
304	6	1.2	162	2	T17035	NADH2 dehydrogenas	377	6	1.2	194	2	T45625	hypothetical prote
305	6	1.2	162	2	T17041	NADH2 dehydrogenas	378	6	1.2	196	2	AD0004	conserved hypotet
306	6	1.2	162	2	T14250	NADH2 dehydrogenas	379	6	1.2	196	2	T01954	hypothetical prote
307	6	1.2	162	2	T14248	NADH2 dehydrogenas	380	6	1.2	196	2	E90273	conserved hypotet
308	6	1.2	162	2	T14251	NADH2 dehydrogenas	381	6	1.2	196	2	G65039	hypothetical prote
309	6	1.2	162	2	T17040	NADH2 dehydrogenas	382	6	1.2	196	2	E72610	hypothetical prote
310	6	1.2	162	2	T14249	NADH2 dehydrogenas	383	6	1.2	198	2	S21388	type I keratin 48k
311	6	1.2	162	2	T17042	NADH2 dehydrogenas	384	6	1.2	198	2	C28544	methyl coenzyme M
312	6	1.2	162	2	T14257	NADH2 dehydrogenas	385	6	1.2	198	2	D69022	conserved hypotet
313	6	1.2	162	2	T14252	NADH2 dehydrogenas	386	6	1.2	198	2	A75324	hypothetical prote
314	6	1.2	162	2	T17037	NADH2 dehydrogenas	387	6	1.2	198	2	S60923	hypothetical prote
315	6	1.2	162	2	T17034	NADH2 dehydrogenas	388	6	1.2	198	2	E71837	protein-export mem
316	6	1.2	162	2	T17038	NADH2 dehydrogenas	389	6	1.2	199	2	A48513	macrophage 23K str
317	6	1.2	162	2	T17043	NADH2 dehydrogenas	390	6	1.2	199	2	152425	probable thioadox
318	6	1.2	162	2	T17039	NADH2 dehydrogenas	391	6	1.2	199	2	AF0947	probable haloacid
319	6	1.2	162	2	T14254	NADH2 dehydrogenas	392	6	1.2	199	2	B95234	DNA-binding respon
320	6	1.2	162	2	T14253	NADH2 dehydrogenas	393	6	1.2	199	2	D98098	response regulator
321	6	1.2	162	2	T14255	NADH2 dehydrogenas	394	6	1.2	199	2	E96926	uracyl DNA glycosi

395	6	1.2	199	2	H90024	hypothetical prote	468	227	2	C69432	hypothetical prote
396	6	1.2	199	2	AF1303	conserved hypotet	469	228	2	S05439	dnak-type molecula
397	6	1.2	199	2	AF1675	conserved hypotet	470	228	2	E87612	cytochrome c, memb
398	6	1.2	200	2	I51016	proliferation asso	471	229	2	A61133	prolactin precuso
399	6	1.2	200	2	D64405	methyl coenzyme M	472	229	2	A60972	SSU ribosomal prot
400	6	1.2	200	2	E89871	hypothetical prote	473	229	2	F69489	glycine betaine/ca
401	6	1.2	201	2	G64676	protein translocat	474	229	2	F69670	ribosomal protein
402	6	1.2	202	2	G71295	conserved hypotet	475	230	2	S25964	probable permease
403	6	1.2	203	2	S50980	NHP10 protein - ye	476	230	2	H83001	conserved hypotet
404	6	1.2	203	2	T25222	hypothetical prote	477	231	2	F70471	hypothetical prote
405	6	1.2	204	2	T33362	hypothetical prote	478	231	2	S74286	probable permease
406	6	1.2	204	2	T07423	actin - Chlorella	479	232	2	H83122	probable ABC trans
407	6	1.2	205	2	B82754	conserved hypotet	480	232	2	C95294	hypothetical prote
408	6	1.2	205	2	F83075	peptidyl-prolyl ci	481	232	2	T21359	hypothetical prote
409	6	1.2	205	2	H91229	probable phosphata	482	232	2	A84732	hypothetical prote
410	6	1.2	206	2	G86076	probable phosphata	483	233	2	C64429	hypothetical prote
411	6	1.2	206	2	S40829	hypothetical 23.5K	484	234	2	F82213	DNA-binding respon
412	6	1.2	206	2	S15205	superoxide dismuta	485	234	2	F82213	probable beta-keto
413	6	1.2	207	2	T34644	probable membrane	486	235	2	A75501	probable beta-keto
414	6	1.2	207	2	S54128	hypothetical 21.4K	487	235	2	E72805	gp48 protein - Myc
415	6	1.2	208	1	C69093	conserved hypotet	488	236	2	D86778	hypothetical prote
416	6	1.2	208	2	B44261	dnak-type molecula	489	237	2	T15702	hypothetical prote
417	6	1.2	208	2	T16953	hypothetical prote	490	237	2	H84732	hypothetical prote
418	6	1.2	209	2	C44261	dnak-type molecula	491	238	1	DECSI	succinate dehydrog
419	6	1.2	209	2	A44261	dnak-type molecula	492	238	2	E90722	succinate dehydrog
420	6	1.2	209	2	D96755	hypothetical prote	493	238	2	D85573	succinate dehydrog
421	6	1.2	209	2	H85644	hypothetical prote	494	238	2	T11718	hypothetical prote
422	6	1.2	209	2	C90785	probable anti-repr	495	238	2	T24314	hypothetical prote
423	6	1.2	209	2	S76973	hypothetical prote	496	238	2	T37040	hypothetical prote
424	6	1.2	210	2	A83097	probable glutathio	497	239	2	S54837	hypothetical prote
425	6	1.2	211	2	AE0552	probable outer mem	498	240	2	B75187	1-(5-phosphoribos
426	6	1.2	212	2	E87712	amidotransferase H	499	240	2	G72295	pyruvate formate-1
427	6	1.2	213	2	T33352	hypothetical prote	500	240	2	T33698	hypothetical prote
428	6	1.2	214	2	B72658	hypothetical prote	501	240	2	T33698	conserved hypotet
429	6	1.2	214	2	S78307	plastoquinol-plast	502	240	2	T27262	hypothetical prote
430	6	1.2	215	2	I40299	variable outer mem	503	241	2	B87337	hypothetical prote
431	6	1.2	215	2	I64004	hypothetical prote	504	241	2	T27262	hypothetical prote
432	6	1.2	215	2	AB1052	probable hexulose-	505	243	2	S30993	gene 48 protein -
433	6	1.2	216	2	T26669	hypothetical prote	506	243	2	D82583	hypothetical prote
434	6	1.2	217	2	E82609	hypothetical prote	507	244	2	B95166	ABC transporter, A
435	6	1.2	217	2	QOEC24	conserved hypotet	508	244	2	G69299	hypothetical prote
436	6	1.2	218	1	D90960	probable transcrip	509	244	2	T20349	hypothetical prote
437	6	1.2	218	2	E85808	probable 2-compone	510	244	2	T01761	hypothetical prote
438	6	1.2	218	2	AE0749	probable 2-compone	511	245	2	A30154	hypothetical prote
439	6	1.2	218	2	AE0749	invasion response-	512	245	2	E95943	IgE receptor alpha
440	6	1.2	218	2	AE2765	hypothetical prote	513	245	2	B83108	probable choline u
441	6	1.2	219	2	B41886	flagellar membrane	514	245	2	B90261	hypothetical prote
442	6	1.2	221	2	F98146	probable amino-aci	515	245	2	T51081	hypothetical prote
443	6	1.2	221	2	AF3141	hypothetical prote	516	246	2	A38678	mast cell proteina
444	6	1.2	222	2	S10728	calcium channel pr	517	246	2	T25532	hypothetical prote
445	6	1.2	222	2	H70920	hypothetical prote	518	247	2	S45113	granzyme-like prot
446	6	1.2	222	2	D69034	conserved hypotet	519	247	2	A25773	dnak-type molecula
447	6	1.2	223	2	AG1615	betaine/carnitine/	520	247	2	D91066	hypothetical membr
448	6	1.2	223	2	A11252	betaine/carnitine/	521	248	2	AD1218	cobalamin (5'-phos
449	6	1.2	223	2	D84297	hypothetical prote	522	248	2	F72262	ubiquinone/menaqui
450	6	1.2	224	2	T20584	hypothetical prote	523	249	2	T03011	dnac protein homol
451	6	1.2	224	2	G72746	branched-chain ami	524	249	2	AG0618	probable DNA repli
452	6	1.2	224	2	E69277	hypothetical prote	525	249	2	E72646	probable molybdopt
453	6	1.2	224	2	D95335	hypothetical prote	526	250	2	H97448	hemolysin importe
454	6	1.2	225	2	AH0839	probable transcrip	527	250	2	AB2667	hemolysin importe
455	6	1.2	226	2	B69670	choline ABC transp	528	251	1	HVCY	astacin [EC 3.4.24
456	6	1.2	226	2	A84969	hypothetical prote	529	251	2	I57668	luteinizing hormon
457	6	1.2	226	2	T24056	hypothetical prote	530	252	2	T13588	NADH2 dehydrogenas
458	6	1.2	226	2	G75342	hypothetical prote	531	252	2	D85910	unknown protein en
459	6	1.2	226	2	T17328	hypothetical prote	532	252	2	B83801	ABC transporter (p
460	6	1.2	226	2	C72102	ct179 hypothetical	533	253	2	H83417	hypothetical prote
461	6	1.2	226	2	F86519	hypothetical prote	534	254	2	S01100	hemolymph 30K prot
462	6	1.2	226	2	A87664	hypothetical prote	535	254	2	AC2163	hypothetical prote
463	6	1.2	226	2	T35435	probable integral	536	254	2	S35008	modulation protein
464	6	1.2	227	2	T44913	probable serine o-	537	254	2	D83446	hypothetical prote
465	6	1.2	227	2	S77870	dnak-type molecula	538	255	2	T40100	conserved phosduc
466	6	1.2	227	2	B71358	hypothetical prote	539	255	2	A70758	hypothetical prote
467	6	1.2	227	2	T42015	probable RNA polym	540	255	2	T48543	hypothetical prote
										AF0515	DedA family integr

541	6	1.2	256	2	S17662	hemolymph 30K prot	614	1.2	279	2	D84185	hypothetical prote
542	6	1.2	256	2	S23691	erythrocyte membra	615	1.2	279	2	H87917	protein F2809.1 [i
543	6	1.2	256	2	QJ1144	H+-transporting tw	616	1.2	279	2	D90258	hypothetical prote
544	6	1.2	256	2	A35340	H+-transporting tw	617	1.2	280	2	C70696	probable transport
545	6	1.2	257	2	AE3190	3-oxoacyl-(acyl-ca	618	1.2	280	2	AE2026	hypothetical prote
546	6	1.2	257	2	I37532	MHC class II histo	619	1.2	281	2	AD3369	universal stress p
547	6	1.2	258	2	A75618	probable chromosom	620	1.2	282	2	AF0902	dihydropterolate sy
548	6	1.2	259	2	H83920	transcription regu	621	1.2	282	2	D72771	probable bacterioc
549	6	1.2	259	2	D97613	hypothetical prote	622	1.2	282	2	T20402	hypothetical prote
550	6	1.2	259	2	AI2835	N-acetylmuramoyl-L	623	1.2	282	2	AE1530	conserved hypothet
551	6	1.2	260	2	D82366	ubiquinone/menaqui	624	1.2	283	2	T33700	hypothetical prote
552	6	1.2	260	2	A57245	VAMP-binding prote	625	1.2	283	2	T51091	hypothetical prote
553	6	1.2	261	2	S17886	MHC class II histo	626	1.2	283	2	G84457	probable mutr doma
554	6	1.2	261	2	I37531	MHC class II histo	627	1.2	283	2	JC5661	hepatoma-derived g
555	6	1.2	261	2	JC4110	triacylglycerol li	628	1.2	285	2	F83890	sugar transport sy
556	6	1.2	261	2	D96029	probable COA-trans	629	1.2	285	2	B84316	halocyanin precurs
557	6	1.2	261	2	A65029	rhodanese-like pro	630	1.2	285	2	T29832	hypothetical prote
558	6	1.2	261	2	D91052	enhanced serine se	631	1.2	286	2	S73423	spermidine/putresc
559	6	1.2	261	2	AF0823	SseB protein limpo	632	1.2	286	2	JE0417	aminoglycoside-N-a
560	6	1.2	261	2	S63604	homeobox protein.G	633	1.2	286	2	T26657	hypothetical prote
561	6	1.2	261	2	A99421	hypothetical prote	634	1.2	286	2	G75437	conserved hypothet
562	6	1.2	261	2	B95273	hypothetical prote	635	1.2	287	2	S57770	xyloglucan endo-1,
563	6	1.2	262	2	F82959	permease of ABC z1	636	1.2	288	2	B71470	probable kinase -
564	6	1.2	262	2	T34115	hypothetical prote	637	1.2	288	2	T04401	endonuclease (EC 3
565	6	1.2	263	2	S44668	hypothetical prote	638	1.2	288	2	C83518	hypothetical prote
566	6	1.2	264	2	C64701	ZK370.7 protein -	639	1.2	288	2	B43253	zinc finger protei
567	6	1.2	264	2	C90339	hypothetical prote	640	1.2	289	2	S68445	probable glucosami
568	6	1.2	264	2	D69811	conserved hypothet	641	1.2	289	2	S49812	xyloglucan endo-1,
569	6	1.2	264	2	T16271	hypothetical prote	642	1.2	289	2	A34783	myogenesis protein
570	6	1.2	265	2	B64128	hypothetical prote	643	1.2	290	2	D97459	sulfate transport
571	6	1.2	265	2	AI0437	lic-1 protein D -	644	1.2	290	2	AF2677	ABC transporter, m
572	6	1.2	265	2	T34755	hypothetical prote	645	1.2	290	2	S36706	B4 protein - equin
573	6	1.2	266	2	D87265	hypothetical prote	646	1.2	290	2	G71623	rifin PFB0065W - m
574	6	1.2	266	2	S67436	hypothetical prote	647	1.2	290	2	AG2309	hypothetical prote
575	6	1.2	266	2	S40988	hypothetical prote	648	1.2	290	2	AI2460	hypothetical prote
576	6	1.2	266	2	B84848	hypothetical prote	649	1.2	291	2	A98325	dipeptide ABC tran
577	6	1.2	268	2	G70553	hypothetical prote	650	1.2	291	2	AE2958	hypothetical prote
578	6	1.2	268	2	D33465	probable echa10 pr	651	1.2	291	2	D96002	probable sugar upt
579	6	1.2	269	2	S32427	lic-1 protein D -	652	1.2	291	2	E82880	translation elonga
580	6	1.2	269	2	AG3638	triester-phosphate i	653	1.2	291	2	A70512	probable preB prot
581	6	1.2	269	2	A83086	inositol-1(or 4)-m	654	1.2	292	2	S76003	hypothetical prote
582	6	1.2	269	2	T44866	conserved hypothet	655	1.2	292	2	T45680	hypothetical prote
583	6	1.2	269	2	H85896	hypothetical prote	656	1.2	292	2	D97199	probable membrane
584	6	1.2	269	2	T36910	enhanced serine se	657	1.2	292	2	H96784	hypothetical prote
585	6	1.2	269	2	T08811	hypothetical prote	658	1.2	292	2	D71181	hypothetical prote
586	6	1.2	269	2	A96955	hypothetical prote	659	1.2	292	2	AG3524	high-affinity bran
587	6	1.2	270	2	AF1172	cobalt permease [i	660	1.2	293	2	H82184	glycerol-3-phospha
588	6	1.2	270	2	B75325	mannose-specific p	661	1.2	293	2	I39620	hypothetical prote
589	6	1.2	270	2	AD3634	hypothetical prote	662	1.2	295	1	QOSABT	hypothetical prote
590	6	1.2	271	2	E70240	norQ protein limpo	663	1.2	295	2	AG1291	transcription acti
591	6	1.2	272	2	A69961	pfs protein (pfs)	664	1.2	295	2	AI1133	hypothetical prote
592	6	1.2	272	2	S27820	geranyltransf	665	1.2	295	2	S67934	branched-chain ket
593	6	1.2	272	2	H71124	vitelline B2 precu	666	1.2	296	2	A95962	probable SDR famli
594	6	1.2	273	2	G87347	hypothetical prote	667	1.2	297	2	AB3037	hypothetical prote
595	6	1.2	273	2	E70572	flagellin FljO [im	668	1.2	297	2	E64733	nicotinate-nucleot
596	6	1.2	274	2	G83186	hypothetical prote	669	1.2	297	2	A99643	quinolinate phosph
597	6	1.2	275	2	E91102	hypothetical prote	670	1.2	297	2	A85494	quinolinate phosph
598	6	1.2	275	2	A85948	probable enzyme [i	671	1.2	297	2	JL0032	hypothetical 31.7K
599	6	1.2	275	2	F65076	probable enzyme y9	672	1.2	297	2	C82787	hypothetical prote
600	6	1.2	275	2	S402565	hypothetical prote	673	1.2	298	2	A87147	hypothetical prote
601	6	1.2	275	2	H82903	conserved hypothet	674	1.2	298	2	G72531	methyl mycolic aci
602	6	1.2	275	2	D97525	FUN4 protein - yea	675	1.2	299	2	A70948	hypothetical prote
603	6	1.2	276	2	T12552	hypothetical prote	676	1.2	299	2	A98249	probable hpx prote
604	6	1.2	276	2	H86922	hypothetical prote	677	1.2	300	2	S60164	nitrate transport
605	6	1.2	276	2	D87407	probable ABC trans	678	1.2	300	2	E97653	transcription init
606	6	1.2	276	2	H75588	conserved hypothet	679	1.2	300	2	AC2877	RNA polymerase sig
607	6	1.2	277	2	AG3534	conserved hypothet	680	1.2	300	2	G95954	probable dTDP-4-de
608	6	1.2	278	2	T51344	oligopeptide trans	681	1.2	301	1	RDRTB5	cytochrome-b5 redu
609	6	1.2	278	2	T19813	dnaK-type molecula	682	1.2	301	2	E72289	oligopeptide ABC t
610	6	1.2	278	2	C95281	hypothetical prote	683	1.2	301	2	G70613	probable mmaA4 pro
611	6	1.2	278	2	B81384	hypothetical prote	684	1.2	302	2	C72756	probable multiple
612	6	1.2	279	2	E81951	probable transmemb	685	1.2	302	2	AB0416	nicotinate-nucleot
613	6	1.2	279	2	B70115	probable membrane-	686	1.2	302	2	T34398	hypothetical prote
						translation elonga						

687	6	1.2	302	2	F95990	probable transcript	760	6	1.2	323	2	T51621	myb-like protein f
688	6	1.2	302	2	S77382	hypothetical prote	761	6	1.2	323	2	T51645	myb-related transc
689	6	1.2	302	2	D70538	probable pbpB prot	762	6	1.2	323	2	T45531	agaB protein [mpo
690	6	1.2	304	2	C82760	UDP-3-O-[3-hydroxy	763	6	1.2	323	2	S73189	prenyl transferase
691	6	1.2	304	2	T42554	tegument protein -	764	6	1.2	323	2	H70765	hypothetical prote
692	6	1.2	304	2	T45469	cell wall lipoprot	765	6	1.2	324	2	A83584	conserved hypothet
693	6	1.2	304	2	T10212	hypothetical prote	766	6	1.2	325	2	C89844	hypothetical prote
694	6	1.2	305	2	JC5361	deoxyribonuclease	767	6	1.2	326	1	QRECB	vitamin B12 transp
695	6	1.2	305	2	B87499	oxidoreductase, Gf	768	6	1.2	326	2	AC0705	vitamin B12 transp
696	6	1.2	307	2	AE0432	conserved hypothet	769	6	1.2	326	2	F85779	vitamin B12 transp
697	6	1.2	307	2	A20852	catechol 2,3-dioxy	770	6	1.2	326	2	B90931	hypothetical prote
698	6	1.2	307	2	S47421	catechol 2,3-dioxy	771	6	1.2	326	2	H72472	hypothetical prote
699	6	1.2	307	2	JC5654	conserved hypothet	772	6	1.2	326	2	C71426	hypothetical prote
700	6	1.2	307	2	G90195	catechol 2,3-dioxy	773	6	1.2	326	2	S61517	fidJin-1 precursor
701	6	1.2	307	4	S58112	hypothetical prote	774	6	1.2	327	1	S45529	NADPH2:quinone red
702	6	1.2	308	2	AE3358	ferric anguibactin	775	6	1.2	327	2	A98258	quinone oxidoreduc
703	6	1.2	308	2	S74719	hypothetical prote	776	6	1.2	327	2	B60988	quinone oxidoreduc
704	6	1.2	308	2	C89866	oligopeptide trans	777	6	1.2	327	2	JC5319	macrolide-lincosam
705	6	1.2	310	2	A24999	L-lactate dehydrog	778	6	1.2	327	2	E72120	transaldolase - Ch
706	6	1.2	310	2	AB3329	tRNA isopentenyltr	779	6	1.2	327	2	C86501	transaldolase (imp
707	6	1.2	310	2	S67181	hypothetical prote	780	6	1.2	327	2	S33672	chain length deter
708	6	1.2	310	2	S58090	probable membrane	781	6	1.2	327	2	AC0765	polysaccharide cha
709	6	1.2	312	2	B70826	probable echA4 pro	782	6	1.2	327	2	AG0062	conserved hypothet
710	6	1.2	312	2	A83486	cobalamin biosynth	783	6	1.2	327	2	S57121	hypothetical prote
711	6	1.2	312	2	AG1302	licheninase (EC 3.	784	6	1.2	328	1	DEHUE7	estradiol 17beta-d
712	6	1.2	312	2	A25455	methionyl-tRNA for	785	6	1.2	328	2	S67570	hypothetical prote
713	6	1.2	312	2	AG1674	transcription regu	786	6	1.2	329	2	S08499	type II DNA modifi
714	6	1.2	312	2	F87615	3-hydroxyisobutyla	787	6	1.2	329	2	H71844	transaldolase CP06
715	6	1.2	313	2	H98227	2-HYDROXY-3-OXOPRO	788	6	1.2	329	2	D81550	hypothetical prote
716	6	1.2	313	2	AH3058	hypothetical prote	789	6	1.2	329	2	D86733	licheninase (EC 3.
717	6	1.2	313	2	S75329	hypothetical prote	790	6	1.2	329	2	S13735	probable cadmium-t
718	6	1.2	314	2	F98231	succinoglycan bios	791	6	1.2	329	2	T05728	ferrichrome ABC tr
719	6	1.2	314	2	AG3054	succinoglycan bios	792	6	1.2	329	2	AC1718	ribosomal protein
720	6	1.2	314	2	T48514	hypothetical prote	793	6	1.2	329	2	AG1347	tryptophanyl-tRNA
721	6	1.2	314	2	AF3621	hypothetical prote	794	6	1.2	330	1	T43816	rlx protein - Stap
722	6	1.2	315	2	T06053	probable ubiquitin	795	6	1.2	330	2	H75505	tRNA isopentenyl t
723	6	1.2	315	2	D83426	hypothetical prote	796	6	1.2	330	2	S28102	hypothetical prote
724	6	1.2	315	2	T15165	hypothetical prote	797	6	1.2	330	2	T48100	cobalamin biosynth
725	6	1.2	315	2	AD2298	hypothetical prote	798	6	1.2	331	2	E86638	hypothetical prote
726	6	1.2	316	2	B83658	phosphoribosyl pyr	799	6	1.2	331	2	B83486	hypothetical prote
727	6	1.2	316	2	C82085	conserved hypothet	800	6	1.2	331	2	H98020	casein Kinase II (
728	6	1.2	316	2	AC1965	proline iminopepti	801	6	1.2	332	2	S19726	probable sugar upt
729	6	1.2	316	2	T44749	hypothetical prote	802	6	1.2	332	2	D95973	Terc family protei
730	6	1.2	316	2	G98184	oligopeptide ABC t	803	6	1.2	332	2	H87705	probable ABC trans
731	6	1.2	316	2	AC3102	hypothetical prote	804	6	1.2	333	2	AI0050	flagellar P-ring p
732	6	1.2	317	2	T18695	hypothetical prote	805	6	1.2	333	2	T37871	hypothetical nucle
733	6	1.2	317	2	S18299	exoz protein - Rhi	806	6	1.2	333	2	F90243	conserved hypothet
734	6	1.2	317	2	E69195	conserved hypothet	807	6	1.2	334	2	S13734	licheninase (EC 3.
735	6	1.2	317	2	T16710	hypothetical prote	808	6	1.2	334	2	S36235	licheninase (EC 3.
736	6	1.2	317	2	B95975	acetyltransferase	809	6	1.2	334	2	T19955	hypothetical prote
737	6	1.2	317	2	A95282	ABC transporter, p	810	6	1.2	334	2	T46238	hypothetical prote
738	6	1.2	318	1	D57987	nrfb protein - Esc	811	6	1.2	334	2	A83414	probable transcript
739	6	1.2	318	2	G91260	formate-dependent	812	6	1.2	334	2	D84321	50S ribosomal prot
740	6	1.2	318	2	C86101	formate-dependent	813	6	1.2	335	2	F72404	flagellar motor sw
741	6	1.2	318	2	AG1020	cytochrome c-type	814	6	1.2	335	2	T41426	hypothetical wtf8
742	6	1.2	318	2	T41838	BRO-c - Bombyx mor	815	6	1.2	335	2	T21503	hypothetical prote
743	6	1.2	318	2	E84360	succinate dehydrog	816	6	1.2	335	2	B87590	hypothetical prote
744	6	1.2	318	2	D87506	glycosyl transfera	817	6	1.2	336	2	T16330	hypothetical prote
745	6	1.2	319	1	ERADF3	fiber protein - hu	818	6	1.2	336	2	D71474	probable muramoyl-
746	6	1.2	319	2	T37130	probable transport	819	6	1.2	336	2	G46289	flavoprotein (fpra
747	6	1.2	319	2	A87171	membrane-bound com	820	6	1.2	336	2	S69270	hypothetical prote
748	6	1.2	319	2	H69964	hypothetical prote	821	6	1.2	336	2	T20586	hypothetical prote
749	6	1.2	319	2	C72553	hypothetical prote	822	6	1.2	336	2	T25002	probable ABC-type
750	6	1.2	319	2	F97626	probable transcript	823	6	1.2	337	2	D64896	hypothetical prote
751	6	1.2	320	2	AH2849	transcription regu	824	6	1.2	337	2	B85734	hypothetical prote
752	6	1.2	320	2	S32655	probable D-amino a	825	6	1.2	337	2	E90884	hypothetical prote
753	6	1.2	320	2	T03899	hypothetical prote	826	6	1.2	337	2	T36307	hypothetical prote
754	6	1.2	320	2	A13234	hypothetical prote	827	6	1.2	338	2	A56274	hypothetical prote
755	6	1.2	321	2	T25004	hypothetical prote	828	6	1.2	339	2	S28686	sulfur-regulated 3
756	6	1.2	321	2	D81018	iron(III) ABC tran	829	6	1.2	340	2	T28686	hypothetical prote
757	6	1.2	321	2	E81962	probable membrane	830	6	1.2	341	2	AF1319	ferrichrome ABC tr
758	6	1.2	322	2	C83075	octaprenyl-diphosp	831	6	1.2	341	2	AF1691	probable sugar upt
759	6	1.2	323	2	A34284	NADH2 dehydrogenas	832	6	1.2	341	2	E95970	

833	6	1.2	341	2	B98338	hypothetical 36.0K	906	6	1.2	357	2	S35318	MET22 protein - ye
834	6	1.2	341	2	A82944	hypothetical prote	907	6	1.2	357	2	C42087	a2-phormone recep
835	6	1.2	341	2	C83578	hypothetical prote	908	6	1.2	358	1	T03917	GMP reductase (EC
836	6	1.2	341	2	B83298	conserved hypochet	909	6	1.2	358	2	T36415	probable iron-side
837	6	1.2	341	2	T51957	metalloproteinase	910	6	1.2	358	2	D82989	alginate biosynthe
838	6	1.2	342	2	AE0155	probable ABC trans	911	6	1.2	358	2	B83808	hypothetical prote
839	6	1.2	342	2	G84885	probable metallopr	912	6	1.2	358	2	F98289	lps biosynthesis r
840	6	1.2	342	2	T44043	hypothetical prote	913	6	1.2	359	1	OKKWC1	protein kinase (EC
841	6	1.2	342	2	T44229	hypothetical prote	914	6	1.2	359	2	T21211	hypothetical prote
842	6	1.2	342	2	T29115	hypothetical prote	915	6	1.2	359	2	A57718	pheromone receptor
843	6	1.2	342	2	T77461	luteinizing hormon	916	6	1.2	359	2	B59105	hypothetical prote
844	6	1.2	342	2	A98309	iron(III) ABC tran	917	6	1.2	360	2	H82081	phospho-N-acetylmu
845	6	1.2	342	2	AE2974	hypothetical prote	918	6	1.2	360	2	B83063	peptide chain rele
846	6	1.2	343	2	D71509	probable proteinas	919	6	1.2	360	2	S36750	cannabinoid recept
847	6	1.2	343	2	F95971	probable exported	920	6	1.2	360	2	G90269	transposase ISC125
848	6	1.2	343	2	AH3159	replication protei	921	6	1.2	360	2	C84243	asparagine synthet
849	6	1.2	344	2	T17056	NADH2 dehydrogenas	922	6	1.2	360	2	S09552	nodulin - soybean
850	6	1.2	344	2	H86503	cytochrome oxidase	923	6	1.2	360	2	JE0116	zinc-finger protei
851	6	1.2	344	2	G72119	cytochrome D ubiqu	924	6	1.2	361	2	B84716	hypothetical prote
852	6	1.2	344	2	C97381	glucokinase (gluco	925	6	1.2	361	2	T42517	bromodomain protei
853	6	1.2	344	2	AB2599	glucokinase [impor	926	6	1.2	362	1	F64302	cobalamin biosynth
854	6	1.2	344	2	T01629	probable GDSL-moti	927	6	1.2	362	2	S17285	hypothetical prote
855	6	1.2	344	2	D84450	hypothetical prote	928	6	1.2	362	2	A71269	conserved hypochet
856	6	1.2	345	2	T17062	NADH2 dehydrogenas	929	6	1.2	363	2	A31342	fructose-bisphosph
857	6	1.2	345	2	T34031	hypothetical prote	930	6	1.2	363	2	T10638	probable riboflavi
858	6	1.2	345	2	T22964	hypothetical prote	931	6	1.2	363	2	T27335	hypothetical prote
859	6	1.2	345	2	T29243	hypothetical prote	932	6	1.2	364	2	E82159	probable periplasm
860	6	1.2	346	2	C59830	glucanase homolog	933	6	1.2	365	2	E87004	conserved hypochet
861	6	1.2	346	2	D72705	hypothetical prote	934	6	1.2	365	2	A84056	hypothetical prote
862	6	1.2	346	2	T09927	cytidine deaminase	935	6	1.2	365	2	H98217	nspC protein (AE00
863	6	1.2	346	2	T19676	hypothetical prote	936	6	1.2	365	2	AC3069	carboxynorspermid
864	6	1.2	346	2	AG1144	conserved hypochet	937	6	1.2	365	2	AG3450	carboxynorspermid
865	6	1.2	346	2	AG1503	conserved hypochet	938	6	1.2	366	1	D70351	probable hexosyltr
866	6	1.2	346	2	T24516	hypothetical prote	939	6	1.2	366	1	SZB55E	stage V sporulatio
867	6	1.2	347	2	E81154	heat shock protein	940	6	1.2	367	2	T35929	probable alcohol d
868	6	1.2	347	2	S70364	cannabinoid recept	941	6	1.2	367	2	T33119	hypothetical prote
869	6	1.2	347	2	G96741	unknown protein F1	942	6	1.2	367	2	JE0349	interferon-inducib
870	6	1.2	347	2	T06671	hypothetical prote	943	6	1.2	367	2	S69586	hypothetical prote
871	6	1.2	347	2	A12310	hypothetical prote	944	6	1.2	367	2	A83681	ABC transporter (p
872	6	1.2	348	2	I50107	MHC class I histoc	945	6	1.2	368	1	QOBEPA	gene 59 protein -
873	6	1.2	349	2	B83434	translocation prot	946	6	1.2	368	2	C70786	probable liveE prot
874	6	1.2	349	2	AD0990	probable membrane	947	6	1.2	368	2	T44887	probable branched-
875	6	1.2	349	2	B99420	hypothetical prote	948	6	1.2	368	2	B84356	AAA-type AtPase [1
876	6	1.2	350	2	AD1555	glucanase and pept	949	6	1.2	369	2	AB2118	UDP-N-acetyl gluc
877	6	1.2	350	2	AF1197	glucanase and pept	950	6	1.2	370	2	D75266	cell division prot
878	6	1.2	350	2	T33798	hypothetical prote	951	6	1.2	371	2	S76682	hypothetical prote
879	6	1.2	350	2	T05589	hypothetical prote	952	6	1.2	371	2	T29154	hypothetical prote
880	6	1.2	350	2	F99883	cell surface prote	953	6	1.2	374	2	B81324	probable ubiquinol
881	6	1.2	350	2	AE3171	ATP-dependent DNA	954	6	1.2	375	1	OKKWC2	protein kinase (EC
882	6	1.2	351	2	D84788	hypothetical prote	955	6	1.2	375	2	T21212	hypothetical prote
883	6	1.2	351	2	S56172	translation initia	956	6	1.2	375	2	D96037	probable ABC trans
884	6	1.2	352	2	S19027	protein kinase A (957	6	1.2	375	2	JN0618	Gal beta 1,3(4)Glc
885	6	1.2	352	2	T39363	RNA binding protei	958	6	1.2	376	2	AE1786	cell division prot
886	6	1.2	353	1	JQ1946	core protein VP7 -	959	6	1.2	376	2	C95878	probable dehydrog
887	6	1.2	353	2	E83577	D-erythrose 4-phos	960	6	1.2	376	2	G84404	hypothetical prote
888	6	1.2	353	2	C31751	protein kinase (EC	961	6	1.2	377	2	C39827	4-coumarate-CoA li
889	6	1.2	353	2	B83848	ferric ion ABC tra	962	6	1.2	377	2	S64687	morphinone reducta
890	6	1.2	353	2	S65086	finger protein XFO	963	6	1.2	377	2	T47791	hypothetical prote
891	6	1.2	353	2	C72479	hypothetical prote	964	6	1.2	377	2	A47380	RING finger-contai
892	6	1.2	354	2	H95011	glycosyl transfera	965	6	1.2	377	2	H89717	protein ClB12.2 l
893	6	1.2	354	2	AB5337	oligopeptide trans	966	6	1.2	378	2	S14959	proline-rich prote
894	6	1.2	355	2	T07160	glutamate-ammonia	967	6	1.2	378	2	JC5245	G protein-coupled
895	6	1.2	356	1	AJAAQ	glutamate-ammonia	968	6	1.2	378	2	C83465	flagellar biosynth
896	6	1.2	356	1	AJFBOB	glutamate-ammonia	969	6	1.2	378	2	B71156	hypothetical prote
897	6	1.2	356	1	AJFBOQ	glutamate-ammonia	970	6	1.2	379	1	A56685	UDPglucose-hexose
898	6	1.2	356	2	TJ1579	glutamate-ammonia	971	6	1.2	379	2	S58452	ubiquinol-cytochro
899	6	1.2	356	2	E84199	hypothetical prote	972	6	1.2	379	2	T11414	ubiquinol-cytochro
900	6	1.2	356	2	B95999	probable iron ABC	973	6	1.2	379	2	A44473	UTP-hexose-1-phosp
901	6	1.2	357	1	QOBE14	BMRF2 protein - hu	974	6	1.2	379	2	I57459	galactose-1-phosph
902	6	1.2	357	2	S36195	glutamate-ammonia	975	6	1.2	379	2	G97265	probable cysteine
903	6	1.2	357	2	F84304	cell division prot	976	6	1.2	379	2	AB2423	hypothetical prote
904	6	1.2	357	2	H98819	conserved hypochet	977	6	1.2	379	2	F91271	hypothetical prote
905	6	1.2	357	2	G75552	riboflavin bifunct	978	6	1.2	379	2	G75170	hypothetical prote

979 6 1.2 379 2 F86112 hypothetical prote
980 6 1.2 380 2 T13758 NADH2 dehydrogenas
981 6 1.2 380 2 T46395 hypothetical prote
982 6 1.2 381 2 T31137 multidrug resistan
983 6 1.2 381 2 C96657 hypothetical prote
984 6 1.2 381 2 T09640 protein phosphatas
985 6 1.2 381 2 T34015 hypothetical prote
986 6 1.2 382 2 D96922 uncharacterized me
987 6 1.2 383 1 VGBKRG glycoprotein precu
988 6 1.2 383 2 T12656 NADH2 dehydrogenas
989 6 1.2 383 2 S53716 delta-like homeoti
990 6 1.2 383 2 B96607 hypothetical prote
991 6 1.2 384 1 BVECCX membrane protein c
992 6 1.2 384 2 T61769 keratin 6d, type I
993 6 1.2 384 2 F85528 cyanate transport
994 6 1.2 384 2 B90678 cyanate transport
995 6 1.2 385 1 S29844 transforming prote
996 6 1.2 385 2 A91006 probable transport
997 6 1.2 385 2 B85850 probable transport
998 6 1.2 385 2 C97883 conserved hypothet
999 6 1.2 385 2 A64981 yehy protein - Esc
1000 6 1.2 386 2 A57066 prostacyclin recep

ALIGNMENTS

RESULT 1
E69791
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
R:Accession: E69791
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
teck, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69791
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-655 <RUN>
A:Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CABL2454.1; PID:el182614;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yebA

Query Match 1.8%; Score 9; DB 2; Length 655;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 VLAVLLVAA 439
|||||||
Db 565 VLAVLLVAA 573

RESULT 2
T36146
hypothetical protein SCE19_23c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36146

R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21598
A:Accession: T36146
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-224 <SEE>
A:Cross-references: EMBL:AL096852; PIDN:CAB51004.1; GSPDB:GN00070; SCOEDB:SCE19.23c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCE19.23c

Query Match 1.6%; Score 8; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 GIVLAVLL 436
|||||||
Db 132 GIVLAVLL 139

RESULT 3
T30232
methyltransferase homolog - Streptomyces hygroscopicus
C:Species: Streptomyces hygroscopicus
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C:Accession: T30232
R:Aparicio, J.F.; Molnar, I.; Schwecke, T.; Koenig, A.; Haydock, S.F.; Khaw, L.E.; St
Gene 169, 9-16, 1996
A:Title: Organization of the biosynthetic gene cluster for rapamycin in Streptomyces
A:Reference number: Z20782; MUID:96186896; PMID:8635756
A:Accession: T30232
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-317 <A>
A:Cross-references: EMBL:X86780; NID:g987088; PID:g987106; PIDN:CAA60466.1
C:Genetics:
A:Gene: rapM

Query Match 1.6%; Score 8; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LREAARAL 19
|||||||
Db 188 LREAARAL 195

RESULT 4
E84280
hypothetical protein Vng1250h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84280
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84280
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-363 <STO>
A:Cross-references: GB:AE004437; NID:gl0580777; PIDN:AAG19609.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG1250H

Query Match 1.6%; Score 8; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 LAVLLVAA 439
 |||||
 Db 17 LAVLLVAA 24

RESULT 5

C41903
 A:Title: arsenical pump membrane protein - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
 C:Accession: C41903
 R:Ji, G.; Silver, S.
 J. Bacteriol. 174, 3684-3694, 1992
 A:Title: Regulation and expression of the arsenic resistance operon from Staphylococcus
 A:Reference number: A41903; MUID:92276351; PMID:1534328
 A:Contents: p1258
 A:Accession: C41903
 A:Molecule type: DNA
 A:Residues: 1-429 <J11>
 A:Cross-references: GB:M86824; NID:g150725; PIDN:AAA25637.1; PID:g150728
 A:Note: sequence extracted from NCBI backbone (NCBIN:104669, NCBIP:104672)
 C:Genetics:
 A:Gene: arsB
 C:Superfamily: arsenical pump membrane protein
 C:Keywords: toxic oxyanion resistance; transmembrane protein

Query Match 1.6%; Score 8; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 IVLAVLLV 437
 |||||
 Db 230 IVLAVLLV 237

RESULT 6

E81817
 A:Title: probable sodium/alanine symporter NMA1901 [imported] - Neisseria meningitidis (strain 22
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: E81817
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 J.; Holroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: E81817
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-472 <PAR>
 A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85122.1; PID:g738053
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA1901
 C:Superfamily: sodium-dependent D-alanine/glycine transport protein.

Query Match 1.6%; Score 8; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 VGIVLAVL 435
 |||||
 Db 195 VGIVLAVL 202

RESULT 7

F81058
 A:Title: amino acid symporter, probable NMB1647 [imported] - Neisseria meningitidis (strain MC58
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: F81058
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755; PMID:10710307
 A:Accession: F81058
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-472 <TET>
 A:Cross-references: GB:AE002515; GB:AE002098; NID:g7226894; PIDN:AAF41996.1; PID:g722
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB1647
 C:Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 1.6%; Score 8; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 VGIVLAVL 435
 |||||
 Db 195 VGIVLAVL 202

RESULT 8

T19786
 A:Title: hypothetical protein C36E8.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T19786
 R:Wilkinson, J.; Barlow, K.
 submitted to the EMBL Data Library, August 1994
 A:Reference number: Z19177
 A:Accession: T19786
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-476 <WIL>
 A:Cross-references: EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C36E8.3
 A:Experimental source: clone C36E8
 C:Genetics:
 A:Gene: CESP:C36E8.3
 A:Map position: 3
 A:Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2
 C:Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match 1.6%; Score 8; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 TIATGGFI 159
 |||||
 Db 171 TIATGGFI 178

RESULT 9

T35715
 A:Title: export protein - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C:Accession: T35715
 R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1998
 A:Reference number: Z21548
 A:Accession: T35715
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-483 <MUR>
 A:Cross-references: EMBL:AL021411; PIDN:CAA16207.1; GSPDB:GN00070; SCOEDB:SC7H1.20c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC7H1.20c
 C:Superfamily: lincomycin-resistance protein ImrB

Query Match 1.6%; Score 8; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 VLAVLLVA 438
 |||||
 DB 29 VLAVLLVA 36

RESULT 10
 A12507
 hypothetical protein alr7241 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: A12507
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: A12507
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-562 <KUR>
 A:Cross-references: GB:BA000020; PIDN:BA078325.1; PID:g17135779; GSPDB:GN00180
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr7241
 A:Genome: plasmid

Query Match 1.6%; Score 8; DB 2; Length 562;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 SPYDGLT 381
 |||||
 DB 481 SPYDGLT 488

RESULT 11
 T46517
 hypothetical protein gra-orf12 [imported] - Streptomyces violaceoruber
 C:Species: Streptomyces violaceoruber
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 11-May-2000
 C:Accession: T46517
 R:Ichinose, K.; Bedford, D.J.; Tornus, D.; Bechthold, A.; Bibb, M.J.; Revill, W.P.; Flos
 Chem. Biol. 5, 647-659, 1998
 A:Title: The granaticin biosynthetic gene cluster of Streptomyces violaceoruber Tu22: se
 A:Reference number: Z23045; MUID:99051446; PMID:9831526
 A:Accession: T46517
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-751 <ICH>
 A:Cross-references: EMBL:AJ011500; PIDN:CAA09633.1
 A:Experimental source: strain Tu22
 C:Genetics:
 A:Note: gra-orf12

Query Match 1.6%; Score 8; DB 2; Length 751;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VLREAAAR 18
 |||||
 DB 38 VLREAAAR 45

RESULT 12
 W5WL33
 E5 protein - human papillomavirus type 33
 C:Species: human papillomavirus type 33
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999

C:Accession: A03679
 R:Cole, S.T.; Strebeck, R.E.
 J. Virol. 58, 991-995, 1986
 A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33,
 A:Reference number: A93020; MUID:86200464; PMID:3009902
 A:Accession: A03679
 A:Molecule type: DNA
 A:Residues: 1-75 <COL>
 A:Cross-references: GB:M12732; NID:g333049; PIDN:AAA46962.1; PID:g463181
 C:Superfamily: papillomavirus E5 protein
 C:Keywords: early protein

Query Match 1.4%; Score 7; DB 1; Length 75;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WLLVLVL 12
 |||||
 DB 31 WLLVLVL 37

RESULT 13
 W5WL58
 E5 protein - human papillomavirus type 58
 C:Species: human papillomavirus type 58
 A:Note: host Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
 C:Accession: D36779
 R:Kirii, Y.; Iwamoto, S.; Matsukura, T.
 Virology 185, 424-427, 1991
 A:Title: Human papillomavirus type 58 DNA sequence.
 A:Reference number: A36779; MUID:92024102; PMID:1656594
 A:Accession: D36779
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-76 <KIR>
 A:Cross-references: GB:D90400; NID:g222386; PIDN:BAA31849.1; PID:g3337102
 C:Superfamily: papillomavirus E5 protein
 C:Keywords: early protein

Query Match 1.4%; Score 7; DB 1; Length 76;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WLLVLVL 12
 |||||
 DB 32 WLLVLVL 38

RESULT 14
 S08449
 hypothetical protein 9 - spiroplasma virus 1
 C:Species: spiroplasma virus 1, Spv1
 C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 07-Dec-1999
 C:Accession: S08449
 R:Renaudin, J.; Aulio, P.; Vignault, J.C.; Bove, J.M.
 Nucleic Acids Res. 18, 1293, 1990
 A:Title: Complete nucleotide sequence of the genome of Spiroplasma citri virus Spv1-R
 A:Reference number: S08447; MUID:90206799; PMID:2320423
 A:Accession: S08449
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-78 <REN>
 A:Cross-references: EMBL:X51344; NID:g61993; PIDN:CAA35727.1; PID:g908898
 C:Genetics:
 A:Genetic code: SGC3

Query Match 1.4%; Score 7; DB 2; Length 78;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 VLLVAAI 440
 |||||

Db 5 VLLVAAI 11

RESULT 15

G97758
Hypothetical protein RC0471 [Imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: G97758
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: G97758
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <KUR>
A:Cross-references: GB:AE006914; FIDN:AAL03009.1; PID:gl5619544; GSPDB:GN00173
C:Genetics:
A:Gene: RC0471

Query Match 1.48; Score 7; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 IELDPSK 289

||||||

Db 16 IELDPSK 22

Search completed: April 22, 2003, 16:19:38
Job time : 67 secs

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EMBL; U15199; AAA69973.1; -.
EMBL; AL591782; CAC41432.1; -.
HSSP; P22259; IAQ2

SM6C_RAT	STANDARD;	PRT;	960 AA.
AC	Q9WTL3; Q9WTM6;		
AD	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Semaphorin 6C precursor (Semaphorin Y) (Sema Y).		
DE	SEMA6C OR SEMAY.		
GN	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=Sprague-Dawley; TISSUE=Muscle;		
RC	MEDLINE=99160821; PubMed=10049528;		
RX	Kikuchi K., Chedotal A., Hanafusa H., Ujimasa Y., de Castro F.,		
RA	Goodman C.S., Kimura T.;		
RA	"Cloning and characterization of a novel class VI semaphorin,		
RT	semaphorin Y.,"		
RL	Mol. Cell. Neurosci. 13:9-23(1999).		
CC	-!- FUNCTION: SHOWS GROWTH CONE COLLAPSING ACTIVITY ON DORSAL ROOT		
CC	GANGLION (DRG) NEURONS IN VITRO. MAY BE A STOP SIGNAL FOR THE DRG		
CC	NEURONS IN THEIR TARGET AREAS, AND POSSIBLY ALSO FOR OTHER		
CC	NEURONS. MAY ALSO BE INVOLVED IN THE MAINTENANCE AND REMODELING OF		
CC	NEURONAL CONNECTIONS.		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SEMA Y-L (SHOWN HERE) AND SEMA		
CC	Y-S; ARE PRODUCED BY ALTERNATIVE SPLICING.		
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN MANY REGIONS OF THE DEVELOPING		
CC	NERVOUS SYSTEM, PROBABLY IN NEURONS AND THEIR PRECURSORS, BUT ALSO		
CC	IN NONNEURAL TISSUE SUCH AS IMMATURE MUSCLE AND DERMIS. IN ADULT,		
CC	STRONG EXPRESSION IN THE SKELETAL MUSCLE AND MODERATE EXPRESSION		
CC	IN THE BRAIN. WHERE CEREELLUM SHOWS THE HIGHEST EXPRESSION.		

EXPRESSED IN ALMOST ALL AREAS OF THE CNS.
-!- DEVELOPMENTAL STAGE: DETECTED AT E12 AND FOUND AT MARKEDLY
INCREASED LEVELS AT E15 AND E18 IN BOTH THE HEAD AND THE BODY. AT
BIRTH THE LEVEL DECREASES SIGNIFICANTLY.
-!- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
-!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
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EMBL; AB000817; BAA76293.2; -
EMBL; AB014074; BAA76295.1; -
DR InterPro; IPR001627; Sema.
DR Pfam; PF01403; Sema; 1.
KW Signal; Transmembrane; Multigene family; Neurogenesis; Glycoprotein;
KW Developmental protein; Alternative splicing.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 960 SEMAPHORIN 6C.
FT DOMAIN 24 635 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 636 656 POTENTIAL.
FT DOMAIN 657 960 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 234 541 SEMA.
FT DOMAIN 693 699 POLY-PRO.
FT DOMAIN 783 786 POLY-PRO.
FT CARBOHYD 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 586 617 MISSING (IN ISOFORM SEMA Y-S).
SQ SEQUENCE 960 AA; 102610 MW; C88293C5607E6086 CRC64;
Query Match 3.8%; Score 102; DB 1; Length 960;
Best Local Similarity 19.1%; Pred. No. 2;
Matches 105; Conservative 60; Mismatches 173; Indels 212; Gaps 27;
QY 17 RALSPOQ---GAGHDEPGSGWAAKGTGKGNR-----ARESPGHV-----SE 57
DB 202 RSLGPPPLRSKYDS-----KWLREPHFVYALEHGDHVFYFFREVSVEDAR 248
QY 58 PRTQLS-----QDLGGTILMD-----TLDPNRTVRVEDNHSYV---VS 94
DB 249 LGRVFSRVARVCKKMDGSGPRALDRHWTSLFKLRLNCSVPGDST-----FYFDVLQ 300
QY 95 RLYGSEPHSRE-----ANRQVKIHTLNTHRQASRVVLSDFDFYGHPLRQIYIATGGFTMGDV 112
DB 301 SLTGPNVNLGRSALFGVFTTQNSIPGSACAFYLDLIERGEGFKQRSILDGAWTPVS 360
QY 113 E-----ANRQVKIHTLNTHRQASRVVLSDFDFYGHPLRQIYIATGGFTMGDV 164
DB 361 EDKVPSPRGSCAGVGAALFSSQDLDPDVLFLFK-----AHPLLDPAVP-----PA 408
QY 165 IHR---MLTATQVAPLPMANPNPGYSDNSTVYVF---DNGTVFVQWHDVYLGWEDKGSF 219
DB 409 THOPLTLTSLRALLTOVAVDGMAGPHRNTVILFSGNDGTVL-----KVLPPGGSLG--- 461
QY 220 TFOAALHHDGRIVFAYKEIPMSVPEISSQHEVTKGLSDAFMILNPSDPVPSRRRSIFE 279
DB 462 -----PEPIILEIDAYSHARCSKRS-----PRAARRIL-- 491
QY 280 YHRIELDPK-----VYMSAVFETPLPTCLQRSCDACMSSDLTFNCMSCHVLRQC----- 331
DB 492 --GLELDTEGHRFLFAFPFCIVYLSLRCAHGAQQRSCLASLDPCYCGW-HRFRGCVNIR 548
QY 332 -SSGFD---RYRQEMDYG-CAQEAQRMCEDFDQEDHDSA-----SPDTSFSPVDG 378
DB 549 GPGGTVDTLGTQNESMEHGDQCGATGS-----QSGPGDSAYVLLGPGSPPTSPSSDA 603
QY 379 DLTTTSSSLFIDSLTTEDDTKLNPYAGDGLQNNISPKTKGTPVHLGTIVGTVLAVLVA 438

DB 604 HPGQSQSTL-----GAHTQGVRRDLSPASASRSIPIPIILLACVAAAFALG 648
QY 439 AILLAGIYN 448
DB 649 ASV-SGLLVS 657
RESULT 4
GLI3_XENLA STANDARD; PRT; 1569 AA.
ID GLI3_XENLA
AC Q91660;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc finger protein GLI3 (Neural specific DNA binding protein XGLI3)
DE (XGLI-3).
GN GLI3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97346726; PubMed=9203143;
RA Marine J.C., Bellefroid E.J., Pendeville H., Martial J.A., Pieler T.;
RT "A role for Xenopus Gli-type zinc finger proteins in the early
embryonic patterning of mesoderm and neuroectoderm";
RL Mech. Dev. 63:211-225(1997).
CC -!- FUNCTION: HAS AN ESSENTIAL ROLE IN THE EARLY EMBRYONIC PATTERNING
OF MESODERM AND NEUROECTODERM. IMPLICATED IN THE TRANSDUCTION OF
SHH SIGNAL (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE GLI FAMILY OF C2H2-TYPE ZINC-FINGER
PROTEINS.
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or send an email to license@isb-sib.ch).
EMBL; U42461; AAA98466.1; -
DR HSP; P08151; XGLI.
DR InterPro; IPR000822; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR PRINTS; PR00048; ZINC_FINGER.
DR SMART; SM00355; Znf_C2H2; 5.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 5.
KW Zinc-finger; Metal-binding; DNA-binding; Transcription regulation;
KW Nuclear protein; Repeat.
FT DOMAIN 485 637 ZINC FINGERS.
FT ZN_FING 485 510 C2H2-TYPE.
FT ZN_FING 518 545 C2H2-TYPE.
FT ZN_FING 551 575 C2H2-TYPE.
FT ZN_FING 581 606 C2H2-TYPE.
FT ZN_FING 612 637 C2H2-TYPE.
SQ SEQUENCE 1569 AA; 172594 MW; 71F5DC117A930B82 CRC64;
Query Match 3.8%; Score 101.5; DB 1; Length 1569;
Best Local Similarity 20.9%; Pred. No. 4.4;
Matches 48; Conservative 29; Mismatches 70; Indels 83; Gaps 10;
QY 187 SDNCTVYVDFGVVQWHDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPMSV--- 242
DB 316 SPNSLVITLNSR-----SSSSASCSYGLHAASIPALNFAYQPTVPSLQOMH 364
QY 243 PEISSQHPVKTGLSDAFMILNPSDPVPSRR-----RSIFPHYRIELDPK-----KVTS 292
DB 365 QQINRSQHSIGSAGFCHSPPLLHPAPTFPSQRTIPGIFSVLNPVQVSGPSEAAQNKPTS 424

QY 293 MEAVFT-----PUPCTCQHR-----SCDACSSDLTF- 320
 DB 425 ESASVSTGDLHNKRSKVPEDHPSPGAVCIQDPGTMVLKKEGVKDESKQAEVYVE 484
 QY 321 -NCSCHVLORCSSGFDYRQ-----EWMYDYGCAQE 350
 DB 485 TNCHW-----EGCSREFDQEQVLVHHNNDHGHGKKEFVCRWLD--CSRE 528

RESULT 5

ID PCK_RHILO STANDARD; PRT; 536 AA.
 AC O96CL7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoenolpyruvate carboxylase [ATP] (EC 4.1.1.49) (PEP
 DE carboxylase) (Phosphoenolpyruvate carboxylase) (PEPCK).
 GN PCKA OR MRS096.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OC NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 CC -!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
 CC + CO(2).
 CC -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
 CC FAMILY.

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DR EMBL; AP003005; BAB51604.1; -
 DR InterPro; IPR001272; PEPCK_ATP.
 DR Pfam; PF01293; PEPCK_ATP; 1.
 DR ProDom; PD004723; PEPCK_ATP; 1.
 DR TIGRFAMs; TIGR00224; pckA; 1.
 DR PROSITE; PS00532; PEPCK_ATP; FALSE_NEG.
 KW Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Complete proteome.
 FT NP_BIND 236 243 ATP (BY SIMILARITY).
 SQ SEQUENCE 536 AA; 58035 MW; 8A3E5D3C7E290743 CRC64;

Query Match 3.7%; Score 99.5; DB 1; Length 536;
 Best Local Similarity 23.0%; Pred. No. 1.5;
 Matches 61; Conservative 37; Mismatches 104; Indels 63; Gaps 14;

QY 44 WNRARESP-----GHVSEPDRTQLSDGGGTLMADTLDPNTRRVVEDN--HS 90
 DB 80 WDNKALSPAQETLPADFALAHAKND--LYVDLVGGADAELKLP---TRVTEFAWHS 134
 QY 91 YVSVRLYGPSEPHSRELWVDVAENRSQVKHITLNSNTHQASR--VVLGFDFFPYGHPL 148
 DB 135 LFTIRNLL--IRPKAELGQVPE--MTIIDLPFRADPARHGRSTETVIAVDL-----T 184

QY 149 RQTIATGGFIEMGDVHRLMTATQY-----VAPLMAFNFCYSDNSTVVFDMGT--- 199
 DB 185 RQI-VLIGTSVAGENKKSQVFTMLNVLKQGVMPHCSANEGPAGDAVFFGLSGTGT 243
 QY 200 -----VFVQVDHIVYLOGHEDKGSFTFOAALHHDGRIVFAYKEIPMSV---PEISS 248
 DB 244 TUSADPSRTLIGDDEH---GMGPHGIFNEFGCY-----AKTIKLSAEAEPEIFAT 291
 QY 249 QHPVKTGLSDAFMILNPSDPVPSR 273
 DB 292 TORFGTVLENVLDADGVDFNDGR 316

RESULT 6

ID N170_YEAST STANDARD; PRT; 1502 AA.
 AC P38181;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Nucleoporin NUP170 (Nuclear pore protein NUP170).
 GN NUP170 OR YBL079W OR YBL0725
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RX MEDLINE=96076635; PubMed=7502586;
 RA Obermaier B., Gassenhuber J., Piravandi E., Domdey H.;
 RT "Sequence analysis of a 78.6 kb segment of the left end of
 RT Saccharomyces cerevisiae chromosome II.";
 RL Yeast 11:1103-1112(1995).
 RN [2]
 RP SEQUENCE OF 1262-1502 FROM N.A.
 RC STRAIN=S288c;
 RA Contreras R., Fiers W., Logghe M., Molemans F.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION, AND SEQUENCE OF 117-133 AND 153-166.
 RX MEDLINE=96095775; PubMed=8522578;
 RA Aitchison J.D., Rout M.P., Marelli M., Blobel G., Wozniak R.W.;
 RT "Two novel related yeast nucleoporins Nup170p and Nup157p:
 RT complementation with the vertebrate homologue Nup155p and functional
 RT interactions with the yeast nuclear pore-membrane protein Pom152p.";
 RL J. Cell Biol. 131:1133-1148(1995).
 CC -!- FUNCTION: ESSENTIAL COMPONENT OF NUCLEAR PORE COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Nuclear pore complex.
 CC -!- SIMILARITY: TO YEAST NUP157, AND SOME, TO MAMMALIAN NUP155.

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DR EMBL; X79489; CAA56029.1; -
 DR EMBL; Z35840; CAA84900.1; -
 DR PIR; S45429; S45429.
 DR SGD; S0000175; NUP170.
 DR InterPro; IPR004870; Nup_nucleoporin.
 DR Pfam; PF03177; Nucleoporin; 1.
 KW Nuclear protein; Transport.
 SQ SEQUENCE 1502 AA; 169474 MW; 3BEA65DAA2A5F99A CRC64;

Query Match 3.6%; Score 98; DB 1; Length 1502;
 Best Local Similarity 22.7%; Pred. No. 8.2;
 Matches 62; Conservative 41; Mismatches 106; Indels 64; Gaps 14;

QY 61 TQLSQDLGGGTLMADTLDPNTRRVVEDNHSYVSRLYGSPHSELWVDVAENRSQVK 120

Db 778 TRLRLDINGRHFVEM-TFTDNRV-----TSHAFISS--DPITPSNNLKSDEISONRNII- 829
 QY 121 IHTILSNTHRASRVLSFD-PPYGHPLROITATTGCFPMGDVVIHRLMTATQYVAP-L 178
 Db 830 -----SKVSTSKDCIEY--LSSINILNEFFITYGDSI-----SQISAPYV 868
 QY 179 MANFNPGYSNDSTVVYFD-----NGTVFVQWHDVYVLOGWEDKGSFTFOAALHHDGRI 231
 Db 869 LANNNGRVIDKTEVANAQASIAINAMIKVQ-----SIKEGLSFLNVLVYSEV 919
 QY 232 -----VFAYKEIPMSVPEISSHPVKTLGSDAFMLNPSDPVPESSRRRSIFYHRIEL 285
 Db 920 EGFNOYLGFKDI-ISFVSLDVQKDLVKLDFKDLF-----APNDKTKSLIREILLSI 970
 QY 286 DPSKVTSMSAVEFTPLPTCLOHRSKDCACMSDDL 318
 Db 971 INRNITKASIEYT--ATALQERCGSCFASDI 1001

RESULT 7
 ID PLX4_HUMAN STANDARD; PRT; 1871 AA.
 AC P51805;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plexin A3 precursor (Plexin 4) (Transmembrane protein sex).
 GN PLXNA3 OR PLXNA4 OR SEX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Fetal brain, Skeletal muscle, and Embryo;
 RC MEDLINE=96149362; PubMed=8570614;
 RA Maestri E., Tamagnone L., Longati P., Cremona O., Gullisano M.,
 RA Bione S., Tamagnini F., Neel B.G., Toniolo D., Conoglio P.M.;
 FT "A family of transmembrane proteins with homology to the MET-
 FT hepatocyte growth factor receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:674-678(1996).
 CC -!- FUNCTION: PUTATIVE RECEPTOR INVOLVED IN THE DEVELOPMENT OF NEURAL
 CC AND EPITHELIAL TISSUES.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: PREDOMINANT IN NEURAL TISSUE DURING
 CC DEVELOPMENT (BY SIMILARITY); WIDELY EXPRESSED IN ADULT TISSUE.
 CC -!- SIMILARITY: WITH THE EXTRACELLULAR DOMAIN OF THE MET/RON/HGF
 CC RECEPTORS AND THE CYTOPLASMIC DOMAIN OF SEP, NOV AND OCT.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X87852; CA61132.1; -
 CC Genew; HGNC:9101; PLXNA3.
 CC MIM; 300022; -
 DR InterPro; IPR002909; IPT_TIG.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR Pfam; PF01437; PSI; 3.
 DR Pfam; PF01833; TIG; 4.
 DR SMART; SM00429; IPT; 4.
 DR SMART; SM00423; PSI; 3.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 1871 PLEXIN A3.

FT DOMAIN 20 1220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1221 1241 POTENTIAL.
 FT DOMAIN 1242 1871 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 738 738 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 746 746 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1009 1009 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1036 1036 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1073 1073 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1115 1115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1162 1162 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1871 AA; 207661 MW; 28420CEBDB22E9CE CRC64;

Query Match 3.6%; Score 98; DB 1; Length 1871;
 Best Local Similarity 24.2%; Pred. No. 11;
 Matches 43; Conservative 25; Mismatches 58; Indels 52; Gaps 10;

QY 160 FMGDVHRLMTATQYV--APLMAENPGYSNDSTVVYFDNGTVFV-----VQWDHVYVLOGW 213
 Db 386 FCGLVLNQPLGGLHVIEGLPLDLADTDGHSVAAYTYRQHSVVFITGRGSLKKVRVDGF 445
 QY 214 EDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSHPVKTLGSDAFMLNPSDPVPESSR 273
 Db 446 QD-----AHLVE-----TPVVDGS--PI---LRDLFF-----SPD----- 471
 QY 274 RRSIFEYHRIELDPKVTSMASVEFTPLPTCLOHRSKDCACMSDDLTFNCSWCHVLCORC 331
 Db 472 HRIHY-----LLSEKQVSQLPFVETCEQYQCAACLGSG-DPHCGWCVLRRHC 517

RESULT 8
 ID IRFL_CHICK STANDARD; PRT; 313 AA.
 AC Q90876;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Interferon regulatory factor 1 (IRF-1).
 GN IRF1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95241453; PubMed=7536924;
 RA Jungwirth C., Rebbert M., Ozato K., Degen H.J., Schultz U.;
 RA David I.B.;
 RT "Chicken interferon consensus sequence-binding protein (ICSBP) and
 RT interferon regulatory factor (IRF) 1 genes reveal evolutionary
 RT conservation in the IRF gene family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109(1995).
 CC -!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF
 CC TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
 CC CONSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE IRF FAMILY.
 CC -----
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 CC -----
 CC EMBL; L39766; AAA62160.1; -
 CC HSPP; P15314; IIF1.
 DR InterPro; IPR001346; IRF.


```

FT DISULFID 852 867 BY SIMILARITY.
FT DISULFID 859 877 BY SIMILARITY.
FT DISULFID 879 890 BY SIMILARITY.
FT DISULFID 896 907 BY SIMILARITY.
FT DISULFID 901 916 BY SIMILARITY.
FT DISULFID 918 929 BY SIMILARITY.
FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 658 658 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 693 693 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 703 703 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 1124 1124 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CONFLICT 44 44 G -> W (IN REF. 3).
FT CONFLICT 54 172 ESSAVKLANPLHFAEYFNSLVNGTNGIISTODFRETOY
VVDYDFDFAIPAFADIDTSHGRGLVREDTSPAVLGL
AARYVRAGFRSARFTTHAFATVEQVAYEEVKRG ->
VKLSRGAGSPALLTKPDSATSWAPTASSPLRTSPGRKS
MTMISPTSRPSPLFWRSTRTATAEASTERTPPQOWA
WPPAMCALASRALRAFYPHPLPGLHAGRLRGQTR
(IN REF. 2 AND 3).
D -> G (IN REF. 1).
FT CONFLICT 453 453
FT SEQUENCE 1375 AA; 151394 MW; 414299D244205FBC CRC64;
Query Match 3.5%; Score 94; DB 1; Length 1375;
Best Local Similarity 19.9%; Pred. No. 16;
Matches 84; Conservative 47; Mismatches 116; Indels 176; Gaps 23;
QY 99 PSE--PHRELMVDVAEANSQVKTHITLSNTHRQASRVV--LSDFPFYGHPLRQIITAT 155
| | | | | : | | | | : | | | | : | |
Db 33 PDELPFHG--ESWGD-----QLLQEGDDESSAVKLANPLHFAEYFNSLVNGT 79
| | | | | : | | | | : | | | | : | |
QY 156 GGFIFMGDVIRMLTATQV-----APLMAFNPCYSNDSTVVYFDNGTVEVVO 204
| | | | | : | | | | : | | | | : | |
Db 80 NGIISTQDFPRE----TQVVDYDFDTPAIPAFADIDTSHG--RGRVLVREDTSPAVLG 134
| | | | | : | | | | : | | | | : | |
QY 205 W-----DHVYLOGWEDKGSF-----TFQAAALHHDGR--- 230
| | | | | : | | | | : | | | | : | |
Db 135 LAARYVRAGFRSARFTTHAFATVEQVAYEEVKRGALPSGELNTFQAVLASGDSY 194
| | | | | : | | | | : | | | | : | |
QY 231 IVFAY-----KE--IPMSVP-----EISSQHVPKT- 254
| | | | | : | | | | : | | | | : | |
Db 195 ALFLYPANGLOFLGTRPKESYNVQLPARVFCRGEADDLKSEGPYSLSTEOSVKNL 254
| | | | | : | | | | : | | | | : | |
QY 255 -GLSD-----AFMLNPSPDVPESRRRSIPEYHRIELD---PSKVTSMGSAVEFT-PLP 302
| | | | | : | | | | : | | | | : | |
Db 255 YQLSNLIGFVNAFHIGTSP-----LDNVYRAAVAGVDSAAHSSVPIG 297
| | | | | : | | | | : | | | | : | |
QY 303 TQLHRSQDACSSDLTLFNCWCHVLQRCSSGFDYRQEWMDYCAQAEAGRMCEDFODE 362
| | | | | : | | | | : | | | | : | |
Db 298 RGFSHAT--ALESD-----YNEDNLDYDVNNEEAAYELPGEPPE 334
| | | | | : | | | | : | | | | : | |
QY 363 D-HDSASPDTSFPYDGLTITSSSLFIDSLTTEDDTKLNPV-----AGDGLQNN 412
| | | | | : | | | | : | | | | : | |
Db 335 ALNGHSSIDVFSQSK-----VDTKPLESSLDLPHTKEGTSLGVEGGPDLQ 382
| | | | | : | | | | : | | | | : | |
QY 413 LSP 415
| | | | | : | | | | : | | | | : | |
Db 383 VEP 385
| | | | | : | | | | : | | | | : | |
RESULT 13
PTPN_MOUSE STANDARD; PRT; 979 AA.
ID PTPN_MOUSE
AC Q60673; Q62129;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Protein-tyrosine phosphatase-like N precursor (R-PTP-N) (PTP IA-2).
GN PTPRN OR Ptp35
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```

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RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95071416; PubMed=7980563;
RA Lu J., Notkins A.B., Lan M.S.;
RT "Isolation, sequence and expression of a novel mouse brain cDNA,
mIA-2, and its relatedness to members of the protein tyrosine
phosphatase family.";
RL Biochem. Biophys. Res. Commun. 204:930-936(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Fibroblast;
RX MEDLINE=96095652; PubMed=8526904;
RA Magistrelli G., Covini N., Mosca M., Lippoli G., Isacchi A.;
RT "Expression of ptp35, the murine homologue of the protein tyrosine
phosphatase-related sequence IA-2, is regulated during cell growth
and stimulated by mitogens in 3T3 fibroblasts.";
RL Biochem. Biophys. Res. Commun. 217:154-161(1995).
CC -1- FUNCTION: IMPLICATED IN NEUROENDOCRINE SECRETORY PROCESSES. MAY BE
INVOLVED IN PROCESSES SPECIFIC FOR NEUROSECRETORY GRANULES, SUCH
AS THEIR BIOGENESIS, TRAFFICKING OR REGULATED EXOCYTOSIS OR MAY
HAVE A GENERAL ROLE IN NEUROENDOCRINE FUNCTIONS. SEEMS TO LACK
INTRINSIC ENZYME ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THE BRAIN AND
FIBROBLASTS. WEAKLY EXPRESSED IN THE COLON, INTESTINE, STOMACH AND
PANCREAS.
CC -1- DEVELOPMENTAL STAGE: IN FIBROBLASTS, MAXIMALLY EXPRESSED IN
EXPONENTIALLY GROWING CELLS (DAYS 1 TO 4).
CC -1- INDUCTION: BY MITOGENS SUCH AS BASIC FIBROBLAST GROWTH FACTOR
(BFGF) AND PLATELET DERIVED GROWTH FACTOR (PDGF).
CC -1- PTM: APPEARS TO UNDERGO MULTIPLE PROTEOLYTIC CLEAVAGE AT
CONSECUTIVE BASIC RESIDUES (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
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or send an email to license@isb-sib.ch).
EMBL; U11812; AAA52102.1;
EMBL; X74438; CAA52453.1; ALT_INIT.
HSP; P29350; IGWZ.
MGD; MGI-102765; Ptpn.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPTASE.
SMART; SM00194; PTPc; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
Receptor; Glycoprotein; Signal; Transmembrane.
SIGNAL 1 37 BY SIMILARITY.
CHAIN 38 979 PROTEIN-TYROSINE PHOSPHATASE-LIKE N.
DOMAIN 38 575 EXTRACELLULAR (POTENTIAL).
TRANSMEM 576 600 POTENTIAL.
DOMAIN 601 979 CYTOPLASMIC (POTENTIAL).
DOMAIN 696 979 PROTEIN-TYROSINE PHOSPHATASE-LIKE.
ACT_SITE 909 909 BY SIMILARITY.
SITE 448 449 CLEAVAGE SITE (BY SIMILARITY).
CARBOHYD 506 506 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 524 524 N-LINKED (GLCNAC. . .) (POTENTIAL).
CONFLICT 166 169 RSWG -> GGGAGA (IN REF. 2).
CONFLICT 363 363 M -> L (IN REF. 2).
CONFLICT 615 615 L -> V (IN REF. 2).
CONFLICT 675 675 S -> T (IN REF. 2).
CONFLICT 859 859 L -> V (IN REF. 2).
SEQUENCE 979 AA; 106087 MW; 99921701B202B8C3 CRC64;
Query Match 3.5%; Score 93.5; DB 1; Length 979;

```

Best Local Similarity 23.0%; Pred. No. 11;
Matches 38; Conservative 23; Mismatches 55; Indels 49; Gaps 7;
QY 275 RSFEYHRELDPSKVTSMASVEFTPLPCLQHRSCDACMSDLTFNC--SNC----- 325
Db 639 KSLFNRAEQOPEFSRVSSVS-QFS-----DAAQSPSSSSPSCSEPAQAN 686
QY 326 -----HVLQRCSSGFDYRQEWMDYGCQAEGRMCEQFQDEHDHDSASPD 370
Db 687 MDISTGHMILAYMEDHLNR-----DRLAKEWQAL-CAVQAEPTNCAAAQDESNIKKNRH 740
QY 371 TSFSPVDG-----DLTTSSSLFDISLTTEDDKLNPAYGGDG 408
Db 741 PDLPLPYDHARIKLVKVESSPSRSDYNASPIIEHPMPAYIATQG 785

RESULT 14

IPCK BRUME STANDARD; PRT; 536 AA.
AC Q8YE41;
DT 15-JUN-2002 (Rel. 41, Last Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP
DE carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).
GN PCKA OR BMEI2037.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapratral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Golsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kypides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
RN [2]
RP CONCEPTUAL TRANSLATION.
RA Coudert E.;
RL Unpublished observations (MAY-2001).
CC -!- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
CC + CO(2).
CC -!- PATHWAY: Rate-limiting gluconeogenic enzyme.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
CC FAMILY.
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A STOP CODON IN
CC POSITION 492 WAS TRANSLATED AS TRP TO RESTORE THE SIMILARITY WITH
CC THE C-TERMINAL REGION OF OTHER HOMOLOGS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AE009636; AAL53218.1; ALT_TERM.
DR InterPro: IPR001272; PEPCK_ATP.
DR Pfam: PF01293; PEPCK_ATP; 1.
DR TIGRfams: TIGR00224; pckA; 1.
DR PROSITE: PS00532; PEPCK_ATP; 1.
DR Glucocorticoidogenesis; Lyase; Decarboxylase; Complete proteome.
FW NP_BIND 236 243 ATP (BY SIMILARITY).
SQ SEQUENCE 536 AA; 58598 MW; 8EC32A1A99FCEA5F CRC64;

Query Match 3.5%; Score 93; DB 1; Length 536;
Best Local Similarity 22.4%; Pred. No. 5.1;
Matches 64; Conservative 41; Mismatches 95; Indels 86; Gaps 15;
QY 65 QDLGGGTAMDTLDPNR--TRVEDN--HSYVV--SRLYGSPSEPHSRELWVDVAEANRSQV 119
Db 110 QDLGGGADA-----DNKINARVITEYAWHSIFIRNLLIRPSQ-----EALASYV 153
QY 120 KIHTILSNTRHQA-----SRVLSDFDPFYGHPLRQITATGTFPMGVHRLMTA 171
Db 154 PENTIIDLPSCADPERYGVRTETVIAVD-----LTRKIVLIGGTSYAGEMKKSVF 206
QY 172 TQY-----VAPLMANPNPGYSDNSTVYVFDNGT-----VFVQWDHVILOGWE 214
Db 207 LNYILPAKGYWPHCSANEGPNDGTAVFFGLSGTGKTTLSADPTRLIGDDEH----GWG 262
QY 215 DKSFTFOAALHHDGRIVFAYKEIPMSV-----PEISSQHPVKTLGSDAFMLNPSDPVE 271
Db 263 EHGVSFEGGY-----AKTIRLSAAEPEIYATTQRTGVLENVLDENRQDPDED 314
QY 272 SRRRSIFEXHR--IELD-----PSKVTSMASVEFTPLP 302
Db 315 G---SLTENTRCAYPLDIPNASKSGKGQPKNIIMLTADAFGVMP 357

RESULT 15

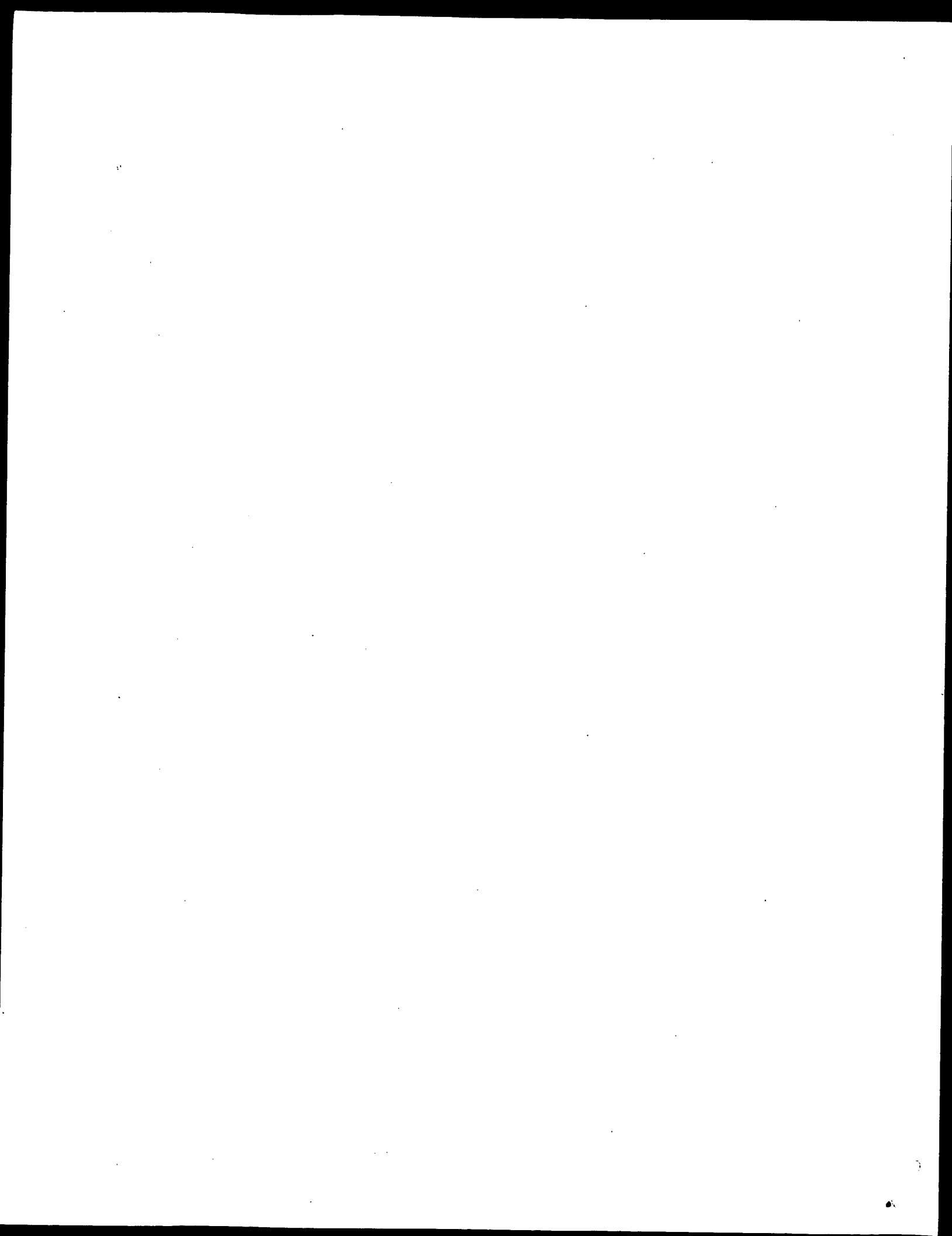
IFHL YEAST STANDARD; PRT; 1085 AA.
AC P39520;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE IFH1 protein (RRP3 protein).
GN IFH1 OR RRP3 OR YLR223C OR L8083.9.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FL100;
RX MEDLINE=95304839; PubMed=7785326;
RA Cherel I., Thuriaux P.;
RT "The IFH1 gene product interacts with a fork head protein in
RT Saccharomyces cerevisiae.";
RL Yeast 11:261-270(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favella A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Taich A., Trevisakis E., Vignati D.,
RA Wilcox L., Wohlman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CONTROLS THE PRE-RRNA PROCESSING MACHINERY IN
CC CONJUNCTION WITH FHL1. COULD CONVERT FHL1 FROM A REPRESSOR
CC TO AN ACTIVATOR.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Z29488; CAA82624.1; -.
DR EMBL: U19027; AAB67412.1; -.
DR PIR: S47477; S47477.

DR SGD; S0004213; IPH1.
KW Nuclear protein; Transcription regulation.
FT DOMAIN 122 163 ASP/GLU-RICH (HIGHLY ACIDIC).
SQ SEQUENCE 1085 AA; 122491 MW; BE1C7DEF06213FE0 CRC64;

Query Match 3.5%; Score 93; DB 1; Length 1085;
Best Local Similarity 19.0%; Pred. No. 14;
Matches 88; Conservative 55; Mismatches 152; Indels 168; Gaps 24;

QY 56 SEPDRQLSGLGGTFLAMDTLPDNRKRVVDNHSYVYVRLYGPSPHSRELWVD--VAE 113
Db 333 NEDSHGEIGTDLTGE---DDLPL---LLEEEQNIYSEL-----QNDELSEFDGSIHE 379
QY 114 ANRSQVK--IHTILSNTHRQAS-----RVVLSDFPFYGHPLRQITATGGFIFM 161
Db 380 EGSDPVEDAEAKFLQNEYQNGYDEDEDEDEIMSDFMFIEDP-----KFANLYYY 433
QY 162 GDVHRMLTATQYVAPLMAN-----FNPGYSDNST 191
Db 434 GDGSEPKLSLSTSL-PLMLNDEKLSKLLKKEAKKREQERKORRKLKKTOKPSTRITSN 492
QY 192 VVYFDNGTVFVQWQHWYLGQWEDKGSFTFQAALHHHGRIVPAYK-----EIPMSVPEISS 247
Db 493 V---DNDEYTF---NVFQSDDENSGHKSKKGRHKSCKSHIEHKNKGNLKSNDLLEP 545
QY 248 SQHP--VKTGLSDFAMILNPSDPVPSRRRSIFEYHRIELDPKVTSMKSAVEFTPLPTCL 305
Db 546 STHSTVLNKGKYS-----SDD-----EYDNILLD-----VAHMP----- 575
QY 306 QHRSCDACMSDLTFNCWCHVLQRCSSGFDYRQEWMDYGCQAEGRAEGRMCEDFQDEHDH 365
Db 576 ---SDDECESESTSHDADTEELRALDS-----DSLIGT-----ELDDDYEDDDDD 619
QY 366 SA-----SPDTFSFSDYGD-----LTTTSS-----LFDLSL 392
Db 620 SSVTNVFIDIDDLDPDSFYHYDSGSSSLISSNSDKNSDGSKCKCKHDLLETIVVYVDDE 679
QY 393 TTEDDTKLNYPAGGDLQNNLSPKTKG-----TPVHLGT 426
Db 680 STDEEDNLPP---PSSRSKNIGSKAKEIVSSNVVGLRPPKLG 719

Search completed: April 22, 2003, 16:07:09
Job time : 31 secs



GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:08:50 ; Search time 14 Seconds
(without alignments)
1481.297 Million cell updates/sec

Title: US-09-918-715-230
Perfect score: 500
Sequence: 1 MRGELWLLVLREARALS.....YAEVPSGHEKGFMEAEQC 500

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.6	429	1 ARSB_STAAU	P30329 staphylococ
2	7	1.4	75	1 V55_HPV33	P06426 human papil
3	7	1.4	76	1 V55_HPV58	P26552 human papil
4	7	1.4	78	1 VG9_SPV1R	P15900 spiroplasma
5	7	1.4	106	1 VMEM_CVB	P37989 chrysanthem
6	7	1.4	120	1 GADP_PIG	P94195 sus scrofa
7	7	1.4	225	1 VME1_IBV6	P05136 avian infec
8	7	1.4	225	1 VME1_IBV6	P04327 avian infec
9	7	1.4	225	1 VME1_IBV6	P11222 avian infec
10	7	1.4	225	1 VME1_IBV6	P12649 avian infec
11	7	1.4	237	1 VG16_BPPEC	P40419 bacillus me
12	7	1.4	286	1 YCXB_BACME	P52532 human herpe
13	7	1.4	342	1 V084_HSV60	P35671 salmonella
14	7	1.4	372	1 INVE_SALTY	P09248 helicobacte
15	7	1.4	388	1 FTSW_HELPJ	P56096 helicobacte
16	7	1.4	388	1 FTSW_HELPJ	P98070 oryctolagus
17	7	1.4	397	1 S17A_RABIT	P58079 caulobacter
18	7	1.4	401	1 HUTI_CAUCR	P09455 agrobacteri
19	7	1.4	407	1 HUTI_AGRRH	P09311 rhizobium l
20	7	1.4	409	1 HUTI_RHIME	P31196 rhizobium m
21	7	1.4	415	1 HUTI_RHIME	P29043 homo sapien
22	7	1.4	417	1 HS47_HUMAN	P19324 mus musculu
23	7	1.4	417	1 HS47_MOUSE	P29457 rattus norv
24	7	1.4	417	1 HS47_MOUSE	P50454 homo sapien
25	7	1.4	418	1 CBP2_HUMAN	P35531 shigella fl
26	7	1.4	430	1 SPAL_SHIFL	P48723 homo sapien
27	7	1.4	471	1 STCH_HUMAN	P02777 felis silve
28	7	1.4	472	1 CB1R_FELCA	P47746 mus musculu
29	7	1.4	473	1 CB1R_MOUSE	P56971 poephila gu
30	7	1.4	473	1 CB1R_POEGU	P20272 rattus norv
31	7	1.4	473	1 CB1R_RAT	P37677 escherichia
32	7	1.4	498	1 LYXK_ECOLI	P08536 arabidopsis
33	7	1.4	524	1 PIF3_ARATH	

1	Y322_MYCGE	1	558	1.4	7	P47564 mycoplasma
2	DTXH_CORBE	1	560	1.4	7	P00589 corynebact
3	DTX_COROM	1	560	1.4	7	P00587 corynebact
4	DTX_CORBE	1	567	1.4	7	P00588 corynebact
5	DNAX_METTH	1	596	1.4	7	P027351 methanobact
6	DNAX_THEAC	1	613	1.4	7	P50023 thermoplas
7	DNAX_THEVO	1	613	1.4	7	P97788 thermoplas
8	YG4P_YEAST	1	622	1.4	7	P50078 saccharomyc
9	Y481_HUMAN	1	650	1.4	7	P75069 homo sapien
10	CAOI_HUMAN	1	660	1.4	7	O15067 homo sapien
11	DP3E_RHOCA	1	704	1.4	7	O68045 rhodobacter
12	DNAX_APHHA	1	721	1.4	7	O52960 aphanothece
13	CADC_HUMAN	1	794	1.4	7	P55289 homo sapien
14	YDGH_BACSU	1	826	1.4	7	O43374 homo sapien
15	PTP3_DICDI	1	885	1.4	7	P96706 bacillus su
16	YB85_YEAST	1	989	1.4	7	P54637 dictyostell
17	CIHA_BACTU	1	1120	1.4	7	P38329 saccharomyc
18	LYS5_ECOLI	1	1172	1.4	7	O45748 bacillus th
19	LYS7_ECOLI	1	1216	1.4	7	Q28339 bos taurus
20	LYS9_ECOLI	1	47	1.2	6	P13344 escherichia
21	MTRF_METH	1	47	1.2	6	Q03709 escherichia
22	MTRF_METHM	1	68	1.2	6	P15176 escherichia
23	BLE2_STAAU	1	68	1.2	6	O27226 methanobact
24	RS20_CLOPE	1	83	1.2	6	O50773 methanobact
25	PTHP_NEIMA	1	87	1.2	6	P22491 staphylococ
26	GAC1_CLOAB	1	89	1.2	6	Q8x182 clostridium
27	YBGA_THEMEA	1	95	1.2	6	Q9jqn1 neisseria m
28	APC3_MAFCA	1	98	1.2	6	P58251 clostridium
29	APC3_CANFA	1	99	1.2	6	Q08640 thermotoga
30	DEF6_HUMAN	1	100	1.2	6	P18659 macaca fasc
31	RL4_PIG	1	100	1.2	6	P12279 canis fami
32	Y70A_METUA	1	101	1.2	6	Q01524 homo sapien
33	VMEM_SMVEA	1	102	1.2	6	Q29187 sus scrofa
34	YJEF_BACSU	1	108	1.2	6	P81311 methanococ
35	HS70_HYDOL	1	109	1.2	6	Q00842 strawberry
36	YFBW_ECOLI	1	111	1.2	6	O31553 bacillus su
37	YFBW_SALTY	1	111	1.2	6	Q05945 hydra olig
38	NRG4_MOUSE	1	111	1.2	6	Q47377 escherichia
39	NLT2_BRANA	1	115	1.2	6	P81891 salmonella
40	NLT1_ARATH	1	117	1.2	6	O52328 salmonella
41	NLTD_BRAOL	1	118	1.2	6	Q9wtx4 mus musculu
42	FOLX_ECOLI	1	118	1.2	6	O42615 brassica na
43	ACPM_ARATH	1	119	1.2	6	Q42589 arabidopsis
44	YK63_MYCTU	1	122	1.2	6	Q43304 brassica ol
45	VCL1_PEA	1	122	1.2	6	P80449 escherichia
46	CD59_PAPSP	1	124	1.2	6	P53665 arabidopsis
47	NRML_RAT	1	126	1.2	6	Q10674 mycobacteri
48	SECE_VTBCH	1	126	1.2	6	P28556 pisum sativ
49	VG41_HAEIN	1	126	1.2	6	Q28785 papio sp. (
50	POLG_HCVCE	1	127	1.2	6	P70553 rattus norv
51	SODM_MVCE	1	128	1.2	6	Q9kv36 vibrio chol
52	SODM_MVCE	1	138	1.2	6	P44235 haemophilus
53	SODM_MVCE	1	138	1.2	6	Q28216 cercopithe
54	RBS_OLILU	1	139	1.2	6	P27953 hepatitis c
55	TOLR_HAEIN	1	139	1.2	6	P53643 mycobacteri
56	GLB1_LUCPE	1	142	1.2	6	P53646 mycobacteri
57	RS6_RHOCA	1	144	1.2	6	P53650 mycobacteri
58	AR15_CAEEL	1	146	1.2	6	P14961 olisthodisc
59	PA21_PIG	1	146	1.2	6	P43769 haemophilus
60	LYC_COTJA	1	147	1.2	6	P41260 lucina pect
61	PA21_HUMAN	1	148	1.2	6	O68126 rhodobacter
62	RNP_GERNI	1	148	1.2	6	P91167 caenorhabdi
63	RNP_TATKG	1	148	1.2	6	P00592 sus scrofa
64	RNP_ACOAC	1	149	1.2	6	P00701 coturnix co
65	RNP_ACOAC	1	149	1.2	6	P04054 homo sapien
66	RNP_ACOAC	1	149	1.2	6	Q9wux2 gerbillus n
67	RNP_ACOAC	1	149	1.2	6	Q9wux4 tatera kemp
68	RNP_ACOAC	1	149	1.2	6	Q9aa39 caulobacter
69	RNP_ACOAC	1	149	1.2	6	Q9tt5 acromys cahi
70	RNP_ACOAC	1	149	1.2	6	Q9wux3 leopoldamys
71	RNP_ACOAC	1	149	1.2	6	Q9wux4 uranomyx ru
72	RNP_ACOAC	1	149	1.2	6	Q9wux6 uranomyx ru
73	RNP_ACOAC	1	149	1.2	6	P31446 escherichia

107	6	1.2	1	1	150	1	RNK6_AOTTR	O46528	aotus trivi	180	6	1.2	231	1	YCB2_YEAST	P25556	saccharomyc
108	6	1.2	1	1	150	1	RNS_BOVIN	P00656	bos taurus	181	6	1.2	233	1	YA36_METJA	Q58442	methanococc
109	6	1.2	1	1	150	1	RNS_BOVIN	P00669	bos taurus	182	6	1.2	235	1	VG48_BPMD2	O64238	mycobacteri
110	6	1.2	1	1	150	1	YO24_BHP1	P51726	bacterioph	183	6	1.2	236	1	ALDC_LACIL	P95676	lactococcus
111	6	1.2	1	1	152	1	RNP_RAT	P00684	rattus norv	184	6	1.2	236	1	ALDC_LACIL	P77880	lactococcus
112	6	1.2	1	1	152	1	RNP_RATRT	Q9wux3	rattus norv	185	6	1.2	238	1	HIS4_RHOSH	P07014	eschlerichia
113	6	1.2	1	1	153	1	SORR_PIG	P28220	sus scrofa	186	6	1.2	239	1	HSB_ECOLI	P50936	rhodobacter
114	6	1.2	1	1	153	1	Y721_AGRVI	P70794	agrobacteri	187	6	1.2	243	1	VG48_BPML5	Q05259	mycobacteri
115	6	1.2	1	1	156	1	YQ69_MYCTU	P12840	rattus norv	188	6	1.2	244	1	Y399_ARCFU	Q29848	archaeoglob
116	6	1.2	1	1	157	1	YQ69_MYCTU	P12840	rattus norv	189	6	1.2	245	1	FCE1_RAT	P12371	rattus norv
117	6	1.2	1	1	159	1	YLH7_CAEEL	P24361	caenorhabd1	190	6	1.2	246	1	MCT9_MOUSE	Q35164	mus musculus
118	6	1.2	1	1	161	1	YPMB_ECHGR	P14088	echinococcu	191	6	1.2	246	1	MCT9_MOUSE	Q00356	mus musculus
119	6	1.2	1	1	161	1	YPMB_BACSU	P54396	bacillus su	192	6	1.2	247	1	HS77_HUMAN	P48741	homo sapien
120	6	1.2	1	1	162	1	PHCA_MASLA	P00307	mastigoclad	193	6	1.2	247	1	MCT8_MOUSE	P43430	mus musculus
121	6	1.2	1	1	162	1	PHCA_SYNEL	P50032	synthococcc	194	6	1.2	251	1	ASTA_ASTFL	P07584	astacus flu
122	6	1.2	1	1	163	1	SODM_MYCKA	P50912	mycobacteri	195	6	1.2	254	1	LP3_BOMMO	P09336	bombyx mori
123	6	1.2	1	1	164	1	YFB5_YEAST	P43578	saccharomyc	196	6	1.2	254	1	NODJ_AZOCA	O07757	azorhizobiu
124	6	1.2	1	1	167	1	RNR_BOVIN	P39873	bos taurus	197	6	1.2	254	1	RACD_DICDI	P34150	dictyostell
125	6	1.2	1	1	168	1	QX2_SULAC	P39479	sulfolobus	198	6	1.2	255	1	YJ95_MYCTU	Q10863	mycobacteri
126	6	1.2	1	1	169	1	HUPJ_BRAJA	P48341	bradyrhizob	199	6	1.2	256	1	ATPF_HUMAN	P24539	homo sapien
127	6	1.2	1	1	174	1	NU6M_DROME	P18933	drosophila	200	6	1.2	256	1	ATPF_MOUSE	Q9C9Q7	mus musculus
128	6	1.2	1	1	175	1	T13C_MOUSE	Q9d8d0	mus musculus	201	6	1.2	256	1	ATPF_RAT	P19511	rattus norv
129	6	1.2	1	1	176	1	AROK_CHLPN	Q9d6m1	chlamydia p	202	6	1.2	256	1	L301_BOMMO	Q00802	bombyx mori
130	6	1.2	1	1	182	1	K2C4_BOVIN	P04260	bos taurus	203	6	1.2	258	1	SSEB_ECOLI	P31143	eschlerichia
131	6	1.2	1	1	182	1	MCRC_METVO	P11567	methanococc	204	6	1.2	260	1	VP33_APLCA	Q16843	aplysia cal
132	6	1.2	1	1	185	1	PSAF_PORPU	P51193	porphyra pu	205	6	1.2	261	1	CLDI_HUMAN	P56856	homo sapien
133	6	1.2	1	1	185	1	VCO7_ADE40	O89532	human adeno	206	6	1.2	261	1	GSHI_MOUSE	P31315	mus musculus
134	6	1.2	1	1	189	1	Y006_CHLTR	O84009	chlamydia t	207	6	1.2	261	1	RNG6_HUMAN	P28067	homo sapien
135	6	1.2	1	1	190	1	Y2H5_STRCO	P35925	streptomyce	208	6	1.2	261	1	YFGF_ECOLI	P52045	eschlerichia
136	6	1.2	1	1	192	1	PAAD_CHLTR	O84222	chlamydia t	209	6	1.2	264	1	CLDI_MOUSE	P56857	mus musculus
137	6	1.2	1	1	192	1	SCPA_PENSP	P02636	penaeus sp.	210	6	1.2	264	1	YFLN_BACSU	Q34409	bacillus su
138	6	1.2	1	1	192	1	YD37_SCHPO	Q10271	schizosacch	211	6	1.2	265	1	LICD_HAEIN	P14184	haemophilus
139	6	1.2	1	1	194	1	GSFH_VIBCH	P45774	vibrio chol	212	6	1.2	266	1	C561_CAEEL	P34465	caenorhabdi
140	6	1.2	1	1	195	1	MSA2_RHILLO	Q98dv6	rhizobium l	213	6	1.2	266	1	COX3_MAGGR	Q95840	magnaporthe
141	6	1.2	1	1	196	1	MOBA_STACA	Q97im7	staphylococ	214	6	1.2	269	1	TPIS_MORSP	Q01893	moraxella s
142	6	1.2	1	1	196	1	TSAL_CANAL	Q9y7f0	candida alb	215	6	1.2	271	1	SRPB_HUMAN	Q9V5m8	homo sapien
143	6	1.2	1	1	198	1	MCRC_METTH	O27234	methanobact	216	6	1.2	272	1	ISPA_BACSU	P54383	bacillus su
144	6	1.2	1	1	198	1	MCRC_METTH	P11566	methanobact	217	6	1.2	273	1	FLJO_CAUCR	O52531	caulobacter
145	6	1.2	1	1	198	1	SECG_HELPJ	Q9ZjX2	helicobacte	218	6	1.2	275	1	SE34_YEAST	P39707	saccharomyc
146	6	1.2	1	1	199	1	PDXL_MOUSE	P35700	mus musculus	219	6	1.2	275	1	VGLM_PUUMB	P41264	puumala vir
147	6	1.2	1	1	199	1	PDXL_RAT	Q63716	rattus norv	220	6	1.2	278	1	HM37_CAEEL	Q93356	caenorhabdi
148	6	1.2	1	1	199	1	SECG_HELPY	Q25847	helicobacte	221	6	1.2	279	1	EFTS_BORBU	O51148	borrelia bu
149	6	1.2	1	1	199	1	TDX_TRYBR	Q26695	trypanosoma	222	6	1.2	286	1	AAC8_STRFR	P29809	streptomyce
150	6	1.2	1	1	199	1	YIHX_ECOLI	P32145	eschlerichia	223	6	1.2	286	1	POTC_MYCPN	P75057	mycoplasma
151	6	1.2	1	1	200	1	MCRV_METJA	O58254	methanococc	224	6	1.2	288	1	ISPE_CHLTR	O84810	chlamydia t
152	6	1.2	1	1	200	1	TDX_ONCPY	Q90384	cynops pyr	225	6	1.2	289	1	GNPL_HUMAN	P46926	homo sapien
153	6	1.2	1	1	200	1	TDX_ONCPY	Q91191	oncorhynch	226	6	1.2	289	1	GNPL_MESAU	Q64422	mesocricetu
154	6	1.2	1	1	203	1	NH10_YEAST	Q03435	saccharomyc	227	6	1.2	289	1	GNPL_MOUSE	O88958	mus musculus
155	6	1.2	1	1	203	1	SODE_MYCTU	P17670	mycobacteri	228	6	1.2	289	1	MYOD_XENLA	P13904	xenopus lae
156	6	1.2	1	1	207	1	YSX2_CAEEL	Q10021	caenorhabdi	229	6	1.2	290	1	UL49_HSV4	Q00039	equine herp
157	6	1.2	1	1	213	1	HIS5_CAUCR	P9a231	caulobacter	230	6	1.2	291	1	EFTS_UREPA	Q9ppx5	ureaplasma
158	6	1.2	1	1	215	1	CYB6_ODOSI	P49488	odontella s	231	6	1.2	296	1	NADC_ECOLI	Q35682	mus musculus
159	6	1.2	1	1	215	1	CYB6_SKECO	O96801	skeletonema	232	6	1.2	296	1	YAYQ_RHISN	P30011	eschlerichia
160	6	1.2	1	1	215	1	Y256_HAEIN	P43973	haemophilus	233	6	1.2	296	1	YAYQ_RHISN	P35725	rhizobium s
161	6	1.2	1	1	218	1	UVRY_ECOLI	P07027	eschlerichia	234	6	1.2	300	1	VU84_HSV62	P52533	human herpe
162	6	1.2	1	1	219	1	FLIZ_BACSU	P35536	bacillus su	235	6	1.2	300	1	NC5R_RAT	P20070	rattus norv
163	6	1.2	1	1	222	1	CCG1_RABIT	P19518	oryctolagus	236	6	1.2	300	1	DRNG_MOUSE	P25070	rattus norv
164	6	1.2	1	1	223	1	IF6_SULAC	P38619	sulfolobus	237	6	1.2	302	1	DRNG_MOUSE	P05057	agrobacteri
165	6	1.2	1	1	224	1	NEPL_AERPE	Q9yes9	aeropyrum p	238	6	1.2	302	1	LPXC_XYLPFA	P49423	prochloroco
166	6	1.2	1	1	226	1	FLCA_BUCAY	P57418	buchnera ap	239	6	1.2	304	1	ACCD_SYNP7	Q9pf75	xyella fas
167	6	1.2	1	1	226	1	OPBD_BACSU	P39775	bacillus su	240	6	1.2	305	1	DRNG_HUMAN	Q34776	synthococcc
168	6	1.2	1	1	227	1	MTR2_MOUSE	Q922d1	mus musculus	241	6	1.2	305	1	ACCD_SYNP7	Q13669	homo sapien
169	6	1.2	1	1	227	1	Y173_TREPA	O83203	treponema p	242	6	1.2	307	1	YXEL_PSEPU	P06622	pseudomonas
170	6	1.2	1	1	227	1	Y173_TREPA	O28812	archaeoglob	243	6	1.2	308	1	YXEL_PSEPU	P72855	synthococcc
171	6	1.2	1	1	228	1	HS74_LEIMA	P12077	leishmania	244	6	1.2	310	1	DRNG_MOUSE	O55070	mus musculus
172	6	1.2	1	1	229	1	OPCD_BACSU	O34742	bacillus su	245	6	1.2	310	1	DRNG_MOUSE	O89107	rattus norv
173	6	1.2	1	1	229	1	PRL_CHICK	P14676	gallus gall	246	6	1.2	310	1	LDH_THECA	P06150	thermus cal
174	6	1.2	1	1	229	1	PRL_MELGA	P17572	meleagris g	247	6	1.2	312	1	MIAA_BRUME	O8y129	bruceella me
175	6	1.2	1	1	229	1	RS3_ARCFU	O28360	archaeoglob	248	6	1.2	312	1	FMT_LISIN	Q92125	listeria in
176	6	1.2	1	1	230	1	NEF_SIVAI	P27970	simian immu	249	6	1.2	312	1	GUB2_HORVU	Q8y676	listeria mo
177	6	1.2	1	1	230	1	RT07_MARPO	P26867	marchantia	250	6	1.2	316	1	YIW3_YEAST	P12257	hordeum vul
178	6	1.2	1	1	231	1	DLHH_AQUAE	O67802	aquifex aeo	251	6	1.2	317	1	EXOZ_RHIME	P40587	saccharomyc
179	6	1.2	1	1	231	1	NU4M_BOTLA	O03700	bothriechlis	252	6	1.2	317	1	YK68_CAEEL	P26502	rhizobium m
																P46558	caenorhabdi

253	6	1.2	317	1	YRP2_CABEL	Q09344	caenorhabdi	326	1	BRB2_RABIT	Q28642	oryctolagus
254	6	1.2	318	1	NRFD_ECOLI	P32709	escherichia	327	1	CCR3_MOUSE	O88410	mus musculus
255	6	1.2	319	1	RTBP_ADE03	P04501	human adeno	328	1	CCR3_HUMAN	P49682	homo sapien
256	6	1.2	320	1	PSTC_MYCLE	Q50098	mycobacteri	329	1	GALT_HUMAN	O60755	homo sapien
257	6	1.2	321	1	YOJP_BACSU	P54553	bacillus su	330	1	ILVE_MYCTU	O32954	mycobacteri
258	6	1.2	322	1	MRAY_ENTHR	O07668	enterococc	331	1	ILVE_MYCTU	Q10399	mycobacteri
259	6	1.2	323	1	MYDM_HUMAN	Q96897	homo sapien	332	1	VG59_HSVSU	O88853	mus musculus
260	6	1.2	324	1	PREA_PORPU	P12772	paracentrot	333	1	GALT_MOUSE	O88854	rattus norv
261	6	1.2	325	1	NU1M_PARLI	P51268	porphyra pu	334	1	GALT_MOUSE	O88854	rattus norv
262	6	1.2	326	1	BTUC_MYCTU	Q10685	mycobacteri	335	1	GALT_MOUSE	O88854	rattus norv
263	6	1.2	327	1	BTUC_ECOLI	Q8417	escherichia	336	1	GALT_MOUSE	O88854	rattus norv
264	6	1.2	328	1	BTUC_SALTI	P06609	escherichia	337	1	GALT_MOUSE	O88854	rattus norv
265	6	1.2	329	1	BTUC_SALTI	Q82615	salmonella	338	1	GALT_MOUSE	O88854	rattus norv
266	6	1.2	330	1	FCN1_HUMAN	O00602	homo sapien	339	1	GALT_MOUSE	O88854	rattus norv
267	6	1.2	331	1	FCN1_HUMAN	P14061	homo sapien	340	1	GALT_MOUSE	O88854	rattus norv
268	6	1.2	332	1	DBH1_HUMAN	P28304	escherichia	341	1	GALT_MOUSE	O88854	rattus norv
269	6	1.2	333	1	QOR_ECOLI	Q92998	chlamydia p	342	1	GALT_MOUSE	O88854	rattus norv
270	6	1.2	334	1	TAL_CHLPN	Q04866	salmonella	343	1	GALT_MOUSE	O88854	rattus norv
271	6	1.2	335	1	WZB_SALTY	P47140	saccharomyc	344	1	GALT_MOUSE	O88854	rattus norv
272	6	1.2	336	1	YJ70_YEAST	Q99501	homo sapien	345	1	GALT_MOUSE	O88854	rattus norv
273	6	1.2	337	1	GA22_HUMAN	Q9A095	streptococc	346	1	GALT_MOUSE	O88854	rattus norv
274	6	1.2	338	1	IDT2_STRPY	Q9A095	streptococc	347	1	GALT_MOUSE	O88854	rattus norv
275	6	1.2	339	1	MRAY_LACIA	Q9A095	streptococc	348	1	GALT_MOUSE	O88854	rattus norv
276	6	1.2	340	1	MRAY_LACIA	Q06844	halobacteri	349	1	GALT_MOUSE	O88854	rattus norv
277	6	1.2	341	1	RL3_HALHA	P14491	staphylococ	350	1	GALT_MOUSE	O88854	rattus norv
278	6	1.2	342	1	FLIG_THEMEA	Q9X1M5	thermotoga	351	1	GALT_MOUSE	O88854	rattus norv
279	6	1.2	343	1	EBP2_SCHPO	P28523	zea mays (m	352	1	GALT_MOUSE	O88854	rattus norv
280	6	1.2	344	1	SPI2_MYXVL	O13802	schizosacch	353	1	GALT_MOUSE	O88854	rattus norv
281	6	1.2	345	1	ARGC_PASMU	Q9WPF7	myxoma viru	354	1	GALT_MOUSE	O88854	rattus norv
282	6	1.2	346	1	FLIG_THEMEA	P57907	pasteurella	355	1	GALT_MOUSE	O88854	rattus norv
283	6	1.2	347	1	MRAY_CHLFR	Q9WY63	thermotoga	356	1	GALT_MOUSE	O88854	rattus norv
284	6	1.2	348	1	YDCT_ECOLI	O84762	chlamydia t	357	1	GALT_MOUSE	O88854	rattus norv
285	6	1.2	349	1	IDT2_DEIRA	P77795	escherichia	358	1	GALT_MOUSE	O88854	rattus norv
286	6	1.2	350	1	OTX3_BRARE	Q9I267	delnecococc	359	1	GALT_MOUSE	O88854	rattus norv
287	6	1.2	351	1	SRPA_SYN7	Q90267	brachydanio	360	1	GALT_MOUSE	O88854	rattus norv
288	6	1.2	352	1	GLK_AGR5	Q55025	synecococc	361	1	GALT_MOUSE	O88854	rattus norv
289	6	1.2	353	1	RLA_CABEL	Q8U1V7	agrobacteri	362	1	GALT_MOUSE	O88854	rattus norv
290	6	1.2	354	1	CB2R_MOUSE	O02056	caenorhabdi	363	1	GALT_MOUSE	O88854	rattus norv
291	6	1.2	355	1	VP7_AHSV6	P47936	mus musculus	364	1	GALT_MOUSE	O88854	rattus norv
292	6	1.2	356	1	VP7_AHSV9	O71027	african hor	365	1	GALT_MOUSE	O88854	rattus norv
293	6	1.2	357	1	COLF_ARATH	Q86729	african hor	366	1	GALT_MOUSE	O88854	rattus norv
294	6	1.2	358	1	E2BB_RABIT	P36325	african hor	367	1	GALT_MOUSE	O88854	rattus norv
295	6	1.2	359	1	ROML_BOVIN	Q9FHH8	arabidopsis	368	1	GALT_MOUSE	O88854	rattus norv
296	6	1.2	360	1	KAPC_DROME	Q28690	oryctolagus	369	1	GALT_MOUSE	O88854	rattus norv
297	6	1.2	361	1	YOL7_CABEL	P52205	bos taurus	370	1	GALT_MOUSE	O88854	rattus norv
298	6	1.2	362	1	GLN1_LOTJA	P12370	drosophila	371	1	GALT_MOUSE	O88854	rattus norv
299	6	1.2	363	1	GLN1_MEDSA	Q02334	caenorhabdi	372	1	GALT_MOUSE	O88854	rattus norv
300	6	1.2	364	1	GLN1_VITVI	Q42899	lotus japon	373	1	GALT_MOUSE	O88854	rattus norv
301	6	1.2	365	1	GLN1_VITVI	P04078	medicago sa	374	1	GALT_MOUSE	O88854	rattus norv
302	6	1.2	366	1	GLN2_SOYBN	P04770	phaseolus v	375	1	GALT_MOUSE	O88854	rattus norv
303	6	1.2	367	1	GLN3_PHAVU	P51118	vitis vinif	376	1	GALT_MOUSE	O88854	rattus norv
304	6	1.2	368	1	GLNA_VIGAC	O82560	glycine max	377	1	GALT_MOUSE	O88854	rattus norv
305	6	1.2	369	1	HAL2_YEAST	P00965	phaseolus v	378	1	GALT_MOUSE	O88854	rattus norv
306	6	1.2	370	1	YMR2_EBV	P32289	vigna acon	379	1	GALT_MOUSE	O88854	rattus norv
307	6	1.2	371	1	YMR2_EBV	P52783	pinus sylve	380	1	GALT_MOUSE	O88854	rattus norv
308	6	1.2	372	1	YMR2_EBV	P32179	saccharomyc	381	1	GALT_MOUSE	O88854	rattus norv
309	6	1.2	373	1	YMR2_EBV	P31302	ustilago ma	382	1	GALT_MOUSE	O88854	rattus norv
310	6	1.2	374	1	YMR2_EBV	P03192	epstein-bar	383	1	GALT_MOUSE	O88854	rattus norv
311	6	1.2	375	1	YMR2_EBV	O16294	caenorhabdi	384	1	GALT_MOUSE	O88854	rattus norv
312	6	1.2	376	1	YMR2_EBV	Q9ZTH5	bacillus an	385	1	GALT_MOUSE	O88854	rattus norv
313	6	1.2	377	1	YMR2_EBV	P21137	caenorhabdi	386	1	GALT_MOUSE	O88854	rattus norv
314	6	1.2	378	1	YMR2_EBV	Q99063	ustilago ho	387	1	GALT_MOUSE	O88854	rattus norv
315	6	1.2	379	1	YMR2_EBV	P34972	homo sapien	388	1	GALT_MOUSE	O88854	rattus norv
316	6	1.2	380	1	YMR2_EBV	Q03249	mus musculus	389	1	GALT_MOUSE	O88854	rattus norv
317	6	1.2	381	1	YMR2_EBV	Q9K994	vibrio chol	390	1	GALT_MOUSE	O88854	rattus norv
318	6	1.2	382	1	YMR2_EBV	P04672	glycine max	391	1	GALT_MOUSE	O88854	rattus norv
319	6	1.2	383	1	YMR2_EBV	P42806	pseudomonas	392	1	GALT_MOUSE	O88854	rattus norv
320	6	1.2	384	1	YMR2_EBV	Q9XYN0	schistocerc	393	1	GALT_MOUSE	O88854	rattus norv
321	6	1.2	385	1	YMR2_EBV	P19112	rattus norv	394	1	GALT_MOUSE	O88854	rattus norv
322	6	1.2	386	1	YMR2_EBV	P27716	drosophila	395	1	GALT_MOUSE	O88854	rattus norv
323	6	1.2	387	1	YMR2_EBV	Q60342	methanococc	396	1	GALT_MOUSE	O88854	rattus norv
324	6	1.2	388	1	YMR2_EBV	P07373	bacillus su	397	1	GALT_MOUSE	O88854	rattus norv
325	6	1.2	389	1	YMR2_EBV	Q991X8	sus scrofa	398	1	GALT_MOUSE	O88854	rattus norv

399	6	1.2	426	1	CGED_BACSU	P42092	426	6	1.2	481	1	MM20_BOVIN	O18767	bos taurus
400	6	1.2	426	1	MNTH_MYCLE	Q50103	473	6	1.2	483	1	MM20_PIG	P79287	sus scrofa
401	6	1.2	426	1	STE2_SACKL	P12384	474	6	1.2	485	1	ER24_FUSSO	Q01447	fusarium so
402	6	1.2	427	1	RL4_HUMAN	P36578	475	6	1.2	485	1	MAQ2_AQUAE	O66937	aquifex aeo
403	6	1.2	428	1	GGPE_NEUCR	P24322	476	6	1.2	485	1	YIHO_ECOLI	P32136	eschericchia
404	6	1.2	428	1	YFUD_ECOLI	Q8Yrb0	477	6	1.2	488	1	FLID_XENNE	P056827	xenorhabdus
405	6	1.2	429	1	ENO_ANASP	Q43127	478	6	1.2	488	1	NUAM_ASPAM	P03913	aspergillus
406	6	1.2	430	1	GLN2_ARATH	P24060	479	6	1.2	489	1	MDM2_MOUSE	P23804	mus musculus
407	6	1.2	432	1	GLXA_BRAJA	P24060	480	6	1.2	489	1	YHIP_ECOLI	P36837	eschericchia
408	6	1.2	433	1	CITM_BACSU	Q99538	481	6	1.2	490	1	LIPL_CHICK	P11602	gallus gall
409	6	1.2	433	1	LGMN_HUMAN	P02983	482	6	1.2	490	1	CYSN_RHTR	O33581	rhizobium t
410	6	1.2	433	1	TCR_STRAU	O89017	483	6	1.2	494	1	HEM2_ORYSA	O22101	oryza sativ
411	6	1.2	435	1	LGMN_MOUSE	Q9r0j8	484	6	1.2	494	1	LIPH_RAT	P07867	rattus norv
412	6	1.2	435	1	LGMN_RAT	Q9r0j8	485	6	1.2	494	1	SYE_STRCO	O86528	streptomyce
413	6	1.2	435	1	ORCS_HUMAN	Q9r0j8	486	6	1.2	495	1	CD5_BOVIN	P19238	bos taurus
414	6	1.2	435	1	ORCS_MOUSE	Q9r0j8	487	6	1.2	495	1	ENP2_MOUSE	O55026	mus musculus
415	6	1.2	437	1	HEM1_ARCFU	Q9r0j8	488	6	1.2	497	1	KPYC_ARATH	O65595	arabidopsis
416	6	1.2	438	1	FAS5_RHOFA	Q9r0j8	489	6	1.2	497	1	SR51_HORVU	P49968	hordeum vul
417	6	1.2	438	1	MAT2_PSEAE	P46377	490	6	1.2	497	1	SR52_HORVU	P49969	hordeum vul
418	6	1.2	439	1	MATK_EPTVI	P30071	491	6	1.2	497	1	YOKI_CABEL	Q09285	caenorhabdi
419	6	1.2	439	1	SEAL_SYNPF	P31159	492	6	1.2	498	1	CYSN_RHIME	P56893	rhizobium m
420	6	1.2	440	1	SCAL_DROME	P30052	493	6	1.2	499	1	GAK_MOUSE	O99kY4	mus musculus
421	6	1.2	441	1	DIHR_ACHDO	P16983	494	6	1.2	500	1	C912_ARATH	P11150	homo sapien
422	6	1.2	441	1	HS7C_CABER	P32088	495	6	1.2	500	1	C340_ORYLA	O65790	arabidopsis
423	6	1.2	441	1	YBE6_YEAST	P38193	496	6	1.2	502	1	C4D1_DROME	Q98t91	oryzias lat
424	6	1.2	442	1	XJBI_ECOLI	P32690	497	6	1.2	502	1	Y190_HELPJ	Q98t91	oryzias lat
425	6	1.2	444	1	GAT6_MOUSE	Q61169	498	6	1.2	502	1	X190_HELPJ	Q98t91	oryzias lat
426	6	1.2	445	1	CANA_CANEN	P50477	499	6	1.2	502	1	Y190_HELPJ	Q98t91	oryzias lat
427	6	1.2	445	1	CANA_CANEN	P10562	500	6	1.2	503	1	HS70_PENCI	Q98t91	oryzias lat
428	6	1.2	445	1	YHFM_ECOLI	P45539	501	6	1.2	503	1	HS70_PENCI	Q98t91	oryzias lat
429	6	1.2	447	1	YHFM_ECOLI	P45539	502	6	1.2	505	1	ATPA_ANTSP	P53832	saccharomyc
430	6	1.2	447	1	NAPE_ENTFA	P37062	503	6	1.2	507	1	MOSB_RHIME	Q02848	antithamio
431	6	1.2	448	1	Y260_TREPA	O83284	504	6	1.2	507	1	MOSB_RHIME	Q02848	antithamio
432	6	1.2	449	1	MURD_STRAM	O33595	505	6	1.2	512	1	C4D1_DROME	Q33269	rosophilla
433	6	1.2	449	1	STRK_STRGR	P09401	506	6	1.2	512	1	C4D1_DROME	Q33269	rosophilla
434	6	1.2	452	1	YP59_MYCTU	O50739	507	6	1.2	512	1	GUAA_CHLMO	O16805	drosophila
435	6	1.2	454	1	MNTH_RHILIO	O98199	508	6	1.2	512	1	K2C5_XENLA	Q9pkM3	chlamydia m
436	6	1.2	456	1	YC88_MYCTU	O10614	509	6	1.2	512	1	K2C5_XENLA	P16878	xenopus lae
437	6	1.2	459	1	TCR2_BACSU	P14512	510	6	1.2	516	1	HS70_LEIMA	P17371	vaccinia vi
438	6	1.2	459	1	YMB6_BACSU	Q47134	511	6	1.2	519	1	CP5V_CANAP	P14834	leishmania
439	6	1.2	461	1	DCUC_ECOLI	O34961	512	6	1.2	519	1	DPVS_MOUSE	P43083	candida api
440	6	1.2	461	1	US45_LACLC	Q47134	513	6	1.2	521	1	GLG3_ARATH	Q9eqf5	mus musculus
441	6	1.2	462	1	PRTF_ERWCH	P22865	514	6	1.2	521	1	MCS4_SCHPO	O63150	rattus norv
442	6	1.2	462	1	REGE_RHOSH	P23598	515	6	1.2	522	1	NU62_HUMAN	P55231	arabidopsis
443	6	1.2	462	1	TRPE_LEPBI	Q53068	516	6	1.2	522	1	GLG4_ARATH	P87323	schizosach
444	6	1.2	463	1	Y096_MYCTU	P20463	517	6	1.2	523	1	ASPA_CORGL	P37198	homo sapien
445	6	1.2	465	1	ALST_BACSU	O10892	518	6	1.2	526	1	CH62_CHLPN	O961k1	arabidopsis
446	6	1.2	465	1	LIPL_BOVIN	Q45068	519	6	1.2	526	1	CH62_CHLPN	Q59200	corynebacte
447	6	1.2	465	1	LIPL_CAVPO	P11151	520	6	1.2	529	1	DNB2_ADE02	Q927c9	chlamydia p
448	6	1.2	465	1	MM12_RAT	P11151	521	6	1.2	529	1	DNB2_ADE02	P03264	human adeno
449	6	1.2	468	1	KG3H_DICDI	Q63341	522	6	1.2	529	1	YGA2_ECOLI	P03265	human adeno
450	6	1.2	468	1	K1CX_HUMAN	P08779	523	6	1.2	532	1	FM05_CAVPO	P37013	eschericchia
451	6	1.2	469	1	NOOD_THETH	Q56228	524	6	1.2	532	1	FM05_HUMAN	P49109	cavia porce
452	6	1.2	469	1	SECY_SULSO	Q9ux84	525	6	1.2	532	1	P72_MYCHY	P43326	homo sapien
453	6	1.2	470	1	ROCC_BACSU	P39636	526	6	1.2	532	1	SPG7_DICDI	P55801	mycoplasma
454	6	1.2	470	1	YMP8_CABEL	Q9ux84	527	6	1.2	536	1	SKIP_HUMAN	P22698	dictyosteli
455	6	1.2	471	1	K1CN_HUMAN	P53993	528	6	1.2	537	1	SKIP_HUMAN	Q13573	homo sapien
456	6	1.2	471	1	RBL2_HYDMR	P02533	529	6	1.2	537	1	PIRG_CHLPN	Q13573	homo sapien
457	6	1.2	473	1	K1CP_HUMAN	Q59460	530	6	1.2	538	1	TYR1_MOUSE	Q928u8	chlamydia p
458	6	1.2	473	1	LIPL_MOUSE	P30654	531	6	1.2	543	1	IF3C_EUGGR	P07147	mus musculus
459	6	1.2	474	1	LIPL_RAT	P11152	532	6	1.2	543	1	SGLT_VIBPA	P36177	euglena gra
460	6	1.2	475	1	LIPL_HUMAN	Q06000	533	6	1.2	544	1	CL21_PEA	P96169	vibrio para
461	6	1.2	475	1	LIPL_MUSVI	P06858	534	6	1.2	545	1	CLL1_SOLTU	Q43068	pisum sativ
462	6	1.2	475	1	LIPL_PAPAN	O46647	535	6	1.2	545	1	CLL2_SOLTU	P31685	solanum tub
463	6	1.2	476	1	GLGA_CHLPN	P49060	536	6	1.2	545	1	CH60_PSEPU	P41685	solanum tub
464	6	1.2	477	1	RFAE_ECOLI	Q926v8	537	6	1.2	547	1	DCIP_AZOB	P42145	pseudomonas
465	6	1.2	477	1	YGIU_ECOLI	P76658	538	6	1.2	547	1	CLL1_TOBAR	P51852	azospirillum
466	6	1.2	478	1	GSA_TOBAR	P42590	539	6	1.2	549	1	LIP2_CANRU	Q24145	nicotiana t
467	6	1.2	478	1	LIPL_FELCA	P31593	540	6	1.2	549	1	FAST_HUMAN	P32946	candida rug
468	6	1.2	478	1	LIPL_PIG	P55031	541	6	1.2	549	1	LIP3_CANRU	Q14296	homo sapien
469	6	1.2	478	1	LIPL_SHEEP	Q49923	542	6	1.2	549	1	LIP4_CANRU	P32947	candida rug
470	6	1.2	480	1	GLPT_HAEIN	P29524	543	6	1.2	550	1	LIP5_CANRU	P32948	candida rug
471	6	1.2	481	1	KRI_HSV11	P63335	544	6	1.2	551	1	YCHM_ECOLI	P40877	eschericchia
						P04413	herpes simp					HMEN_DROME	P14784	homo sapien
													P02836	drosophila

545	6	1.2	552	1	K2C6_MOUSE	P50446	mus musculus	618	1.2	610	1	DNAK_STAAU	P45554	staphylococ
546	6	1.2	552	1	YM81_MYCTU	Q50684	mycobacteri	619	1.2	611	1	ADAS_DICTDI	Q96759	dityostel
547	6	1.2	554	1	SERA_SYNY3	P73821	synchocyst	620	1.2	611	1	BCHS_RHOSH	Q9rfd3	rhyobacter
548	6	1.2	555	1	DP87_DICTDI	Q04503	dictyostell	621	1.2	611	1	HSCA_BUCAI	P57660	buchnera ap
549	6	1.2	556	1	HSCC_ECOLI	P77319	escherichia	622	1.2	612	1	DNAK_LISIN	Q92bn8	listeria in
550	6	1.2	557	1	MCP5_ENTAE	P21822	enterobacte	623	1.2	612	1	DNAK_LISMO	Q95544	listeria mo
551	6	1.2	559	1	FLIF_SALTY	P15928	salmonella	624	1.2	612	1	HS75_KLUMA	P41770	kluveromyc
552	6	1.2	563	1	K2CA_HUMAN	P02538	homo sapien	625	1.2	612	1	HS75_YEAST	P40150	saccharomyc
553	6	1.2	563	1	K2CB_HUMAN	P04259	homo sapien	626	1.2	612	1	PLB1_PENCH	P39457	penicillium
554	6	1.2	563	1	K2CC_HUMAN	P48666	homo sapien	627	1.2	612	1	DNAK_BACHD	Q9kd72	bacillus ha
555	6	1.2	563	1	K2CE_HUMAN	P48668	homo sapien	628	1.2	613	1	DNAK_LAGSK	O87777	lactobacill
556	6	1.2	563	1	K2CF_HUMAN	P48669	homo sapien	629	1.2	613	1	HS75_CANAL	P87222	candida alb
557	6	1.2	565	1	DSBD_ECO57	P58162	escherichia	630	1.2	613	1	HS75_SCHPO	Q10284	schizosacch
558	6	1.2	565	1	DSBD_ECOLI	P36655	escherichia	631	1.2	613	1	DNAK_CLOAB	P30721	clostridium
559	6	1.2	567	1	DSBD_SALT1	Q8zla8	salmonella	632	1.2	614	1	DNAK_ODOSI	P49463	odontotelli s
560	6	1.2	567	1	DSBD_SALTY	Q8zxc3	salmonella	633	1.2	614	1	VAAL_DROME	P48602	drosophila s
561	6	1.2	568	1	FLP_ZYGH1	P13784	zygosacchar	634	1.2	614	1	VAA2_DROME	Q27331	drosophila
562	6	1.2	571	1	UGA4_YEAST	P32873	saccharomyc	635	1.2	614	1	DNAK_THETH	Q56235	thermus the
563	6	1.2	571	1	C114_MOUSE	P19467	mus musculu	636	1.2	615	1	VATA_AEDAE	O16109	aedes aegypt
564	6	1.2	573	1	SECD_MYCTU	Q50634	mycobacteri	637	1.2	615	1	HSCA_ECOLI	P36541	escherichia
565	6	1.2	574	1	SPKB_SYNY3	P74297	synchocyst	638	1.2	616	1	TR11_HUMAN	Q9v6q6	homo sapien
566	6	1.2	575	1	COLL_DROME	P56721	drosophila	639	1.2	616	1	DNAK_PROAC	Q917p1	propionibac
567	6	1.2	575	1	FUT8_MOUSE	Q9wts2	m alpha-(1,	640	1.2	617	1	MBHL_ALCEU	P31891	alcaligenes
568	6	1.2	575	1	ML1X_SHEEP	Q28558	ovis aries	641	1.2	617	1	DNAK_CYACA	Q9tlt1	cyandium c
569	6	1.2	578	1	YDEM_CABEL	Q19124	caenorhabdi	642	1.2	618	1	DNAK_DEIPR	P94695	deinococcus
570	6	1.2	578	1	YDV8_SCHPO	O14226	schizosacch	643	1.2	618	1	DNAK_STRCO	Q05558	streptomyc
571	6	1.2	579	1	SDV_THEMEA	Q9x1f4	thermotoga	644	1.2	618	1	DNAK_STRGR	Q54215	streptomyc
572	6	1.2	581	1	PGMD_BRGIN	Q9snx2	bromus iner	645	1.2	619	1	DNAK_CLOPE	P26823	clostridum
573	6	1.2	583	1	PMEO_LYCES	Q43143	lycopersico	646	1.2	619	1	DNAK_HELPJ	Q9zmw4	helicobacte
574	6	1.2	585	1	MECR_STAAM	P26597	staphylococ	647	1.2	619	1	DNAK_HELPY	P55994	helicobacte
575	6	1.2	587	1	HE_PARLI	P22757	paracentrot	648	1.2	619	1	DNAK_METMA	P27094	metanosa
576	6	1.2	588	1	SYD_HAETN	P43817	haemophilus	649	1.2	619	1	DNAK_MYCLE	P19593	mycobacteri
577	6	1.2	588	1	SYD_PASMU	P57895	pasteurella	650	1.2	619	1	HSCA_HAETN	P44669	haemophilus
578	6	1.2	589	1	SIFB_DROME	Q06942	drosophila	651	1.2	619	1	HSCA_PSEAE	Q51382	pseudomonas
579	6	1.2	590	1	DNAK_STRMU	O06942	streptococc	652	1.2	620	1	DNAK_PORPU	P30723	porphyra pu
580	6	1.2	590	1	SYD_ECO57	Q8xc17	escherichia	653	1.2	620	1	NODQ_AZORU	P28604	a nodq bifu
581	6	1.2	590	1	SYD_ECOLI	P21889	escherichia	654	1.2	621	1	MBHL_ALCHY	P33374	alcaligenes
582	6	1.2	590	1	SYD_SALTY	Q8zmv2	salmonella	655	1.2	621	1	MBHL_ALCHY	P33374	alcaligenes
583	6	1.2	590	1	SYD_SALTY	Q8zmv2	salmonella	656	1.2	621	1	MBHL_ALCHY	P33374	alcaligenes
584	6	1.2	591	1	DNAK_MYCCA	P45958	mycoplasma	657	1.2	621	1	MBHL_ALCHY	P33374	alcaligenes
585	6	1.2	593	1	HSCA_RICPR	Q9zdw5	rickettsia	658	1.2	623	1	DNAK_MYCTU	Q9hhb9	halobacteri
586	6	1.2	595	1	BETP_CORGL	P47547	mycoplasma	659	1.2	623	1	DNAK_MYCTU	Q9hhb9	halobacteri
587	6	1.2	595	1	DNAK_MYCGE	P47547	mycoplasma	660	1.2	623	1	DNAK_MYCTU	Q9hhb9	halobacteri
588	6	1.2	595	1	DNAK_MYCGE	P47547	mycoplasma	661	1.2	623	1	DNAK_MYCTU	Q9hhb9	halobacteri
589	6	1.2	595	1	DNAK_MYCPN	P75344	thermotoga	662	1.2	624	1	DNAK_MYCTU	Q9hhb9	halobacteri
590	6	1.2	595	1	DNAK_THEMEA	Q9xyk6	thermotoga	663	1.2	624	1	DNAK_MYCTU	Q9hhb9	halobacteri
591	6	1.2	596	1	MBHL_BRAJA	P12636	bradyrhizob	664	1.2	624	1	DNAK_MYCTU	Q9hhb9	halobacteri
592	6	1.2	596	1	MBHL_RHILV	P18636	rhizobium l	665	1.2	624	1	DNAK_MYCTU	Q9hhb9	halobacteri
593	6	1.2	599	1	ABEL_HUMAN	Q96b10	homo sapien	666	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
594	6	1.2	599	1	DNAK_MYCPU	Q98qy7	mycoplasma	667	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
595	6	1.2	599	1	HS7S_SPTOL	Q08080	spinacia ol	668	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
596	6	1.2	600	1	DNAK_ERYTH	Q05647	erysipeloth	669	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
597	6	1.2	600	1	DNAK_MYCHY	Q49539	mycoplasma	670	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
598	6	1.2	600	1	ESR1_RAT	P06211	rattus norv	671	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
599	6	1.2	602	1	MBHL_AZOV1	P21949	azotobacter	672	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
600	6	1.2	602	1	SYD_RICCN	Q92182	rickettsia	673	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
601	6	1.2	603	1	DNAK_UREPA	Q9pqf2	ureaplasma	674	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
602	6	1.2	604	1	DNAK_BACHE	P05646	bacillus me	675	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
603	6	1.2	605	1	APM2_YEAST	P38700	saccharomyc	676	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
604	6	1.2	605	1	SL51_PIG	P26429	sus scrofa	677	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
605	6	1.2	606	1	KINA_BACSU	Q9kws7	bacillus th	678	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
606	6	1.2	606	1	DNAK_BACST	P16497	bacillus su	679	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
607	6	1.2	607	1	DNAK_LACLA	Q45551	bacillus st	680	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
608	6	1.2	607	1	DNAK_LACLA	P42368	lactococcus	681	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
609	6	1.2	607	1	DNAK_MYXXA	P95334	myxococcu	682	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
610	6	1.2	607	1	DNAK_STRPN	P95829	streptococc	683	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
611	6	1.2	607	1	DNAK_STRPY	P95831	streptococc	684	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
612	6	1.2	608	1	HSCA_BUCAP	O51883	buchnera ap	685	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
613	6	1.2	609	1	DNAK_STRAG	P95693	streptococc	686	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
614	6	1.2	610	1	DNAK_BACSH	O69268	bacillus sp	687	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
615	6	1.2	610	1	DNAK_BACSU	P17820	bacillus su	688	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
616	6	1.2	610	1	DNAK_METTE	Q9uxr0	methanosarc	689	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien
617	6	1.2	610	1	DNAK_STAAM	O99tr7	staphylococ	690	1.2	625	1	DUS8_HUMAN	Q13202	homo sapien

691	6	1.2	636	1	DNAX_EHRSE	085282 ehrlichia s	764	1.2	645	1	HS70_SOYBN	P26413 glycine max
692	6	1.2	636	1	DNAX_YERPE	Q8zim7 yersinia pe	765	1.2	645	1	SUBB_BACSU	P16396 bacillus su
693	6	1.2	636	1	DNK2_SYNY3	P22358 synechocyst	766	1.2	645	1	VP74_NPVAC	P15963 autographa
694	6	1.2	637	1	DNAX_BRUME	Q8ve76 bruceella me	767	1.2	646	1	HS70_NEUCR	Q01233 neurospora
695	6	1.2	637	1	DNAX_BRUCV	Q05981 bruceella ov	768	1.2	646	1	HS70_THEAN	P16019 theileria a
696	6	1.2	637	1	DNAX_BUCAT	Q2464 buchnera ap	769	1.2	646	1	HS7C_CRIGR	P19378 cricetus
697	6	1.2	637	1	DNAX_ECULI	P04475 escherichia	770	1.2	646	1	HS7C_HUMAN	P11142 homo sapien
698	6	1.2	637	1	DNAX_PSEAE	Q9hv43 pseudomonas	771	1.2	646	1	HS7C_MOUSE	P08109 mus musculus
699	6	1.2	637	1	DNAX_RHOCA	Q52701 rhodobacter	772	1.2	647	1	CCMF_ECOLI	P33927 escherichia
700	6	1.2	637	1	DNAX_SALTI	Q829r1 salmonella	773	1.2	647	1	HS70_XENLA	P02827 xenopus lae
701	6	1.2	637	1	DNAX_SALTY	Q56073 salmonella	774	1.2	647	1	VEI_HPV52	P36730 human papil
702	6	1.2	637	1	DNAX_VIBPR	Q917r1 vibrio prot	775	1.2	647	1	YIK1_YEAST	P40489 saccharomyc
703	6	1.2	637	1	HS70_SCHMA	P08418 schistosoma	776	1.2	648	1	HS71_PUCGR	Q01877 puccinia gr
704	6	1.2	638	1	DNAX_PRELO	Q93gfl prevotella	777	1.2	648	1	WHN_HUMAN	O15353 homo sapien
705	6	1.2	638	1	DNAX_PSEEG	Q9w9g9 pseudomonas	778	1.2	649	1	HS70_BLAEM	P48720 blastoclad
706	6	1.2	638	1	DNAX_RHILE	Q33528 rhizobium l	779	1.2	649	1	HS70_CHLRE	P25840 chlamydomon
707	6	1.2	638	1	DNAX_RHIZO	Q98dd1 rhizobium l	780	1.2	649	1	HS70_FARBR	P87047 paracoccidi
708	6	1.2	638	1	DNAX_XYLF	Q9pb05 xyella fas	781	1.2	649	1	HS73_ARATH	P37899 pyrenomonas
709	6	1.2	638	1	HS70_CERCA	Q9pb05 xyella fas	782	1.2	649	1	HS73_YEAST	O65719 arabidopsis
710	6	1.2	638	1	HS71_CERAE	Q28222 cercaritis c	783	1.2	649	1	HS7C_YEAST	P09435 saccharomyc
711	6	1.2	638	1	HS72_YEAST	P10592 saccharomyc	784	1.2	649	1	HS7C_LECTU	P47773 ictalurus p
712	6	1.2	639	1	HS72_ORYLA	P05932 saccharomyc	785	1.2	649	1	PLB1_TORDE	Q11121 torulaspore
713	6	1.2	639	1	HS72_HUMAN	P54652 homo sapien	786	1.2	650	1	DNAX_BURPS	P42373 burkholderi
714	6	1.2	639	1	HS74_PARLI	Q06248 paracentrot	787	1.2	650	1	HS7C_BOVIN	O68191 burkholderi
715	6	1.2	639	1	MET7_YEAST	P47164 saccharomyc	788	1.2	650	1	HS7C_BOVIN	P24629 lycopersico
716	6	1.2	639	1	V70K_PLRWV	P11622 potato leaf	789	1.2	650	1	HS70_OCNMY	P19120 bos taurus
717	6	1.2	640	1	DNAX_PORGI	Q9zad3 porphyromon	790	1.2	651	1	HS7C_OCNMY	P08108 oncorhynch
718	6	1.2	640	1	DNAX_RHOMR	Q9xch1 rhodothermu	791	1.2	651	1	HS71_ARATH	P22953 arabidopsis
719	6	1.2	640	1	DNAX_VIBHA	O87384 vibrio harv	792	1.2	651	1	HS7C_PETHY	P09189 petunia hyb
720	6	1.2	640	1	HS71_ANOAL	P41825 anopheles a	793	1.2	651	1	HS7D_DROME	P11147 drosophila
721	6	1.2	640	1	HS72_ANOAL	P41826 anopheles a	794	1.2	652	1	CD93_HUMAN	Q9np93 homo sapien
722	6	1.2	640	1	HS74_ANOAL	P41827 anopheles a	795	1.2	652	1	GR78_CHICK	Q90593 gallus gall
723	6	1.2	640	1	HS7A_CABEL	P09446 caenorhabdi	796	1.2	652	1	HS70_ACHXL	P41753 achlya kieb
724	6	1.2	640	1	HS7C_DICDI	P36415 dictyosteli	797	1.2	652	1	HS70_LEIAM	O07437 leishmania
725	6	1.2	641	1	DNAX_METSS	Q9zfc6 methylovoru	798	1.2	652	1	HS7D_WANSE	Q9u639 manduca sex
726	6	1.2	641	1	DNAX_RHIME	P42374 rhizobium m	799	1.2	652	1	HS7E_SPIOL	P29357 spinacia ol
727	6	1.2	641	1	HS71_BOVIN	Q27975 bos taurus	800	1.2	653	1	HS70_LEIDO	P17804 leishmania
728	6	1.2	641	1	HS71_HUMAN	P08107 homo sapien	801	1.2	653	1	HS72_ARATH	P22954 arabidopsis
729	6	1.2	641	1	HS71_MOUSE	P17879 mus musculus	802	1.2	654	1	DNAX_CHLMU	P56836 chlamydia m
730	6	1.2	641	1	HS71_PIG	Q07439 rattus norv	803	1.2	654	1	GR78_HUMAN	P11021 homo sapien
731	6	1.2	641	1	HS71_RAT	P10591 saccharomyc	804	1.2	654	1	GR78_MESAU	P07823 mesocricetu
732	6	1.2	641	1	HS72_YEAST	Q27965 bos taurus	805	1.2	654	1	GR78_RAT	P06761 rattus norv
733	6	1.2	641	1	HS72_BOVIN	P02824 drosophila	806	1.2	654	1	HS70_HYDMA	Q05944 hydra magni
734	6	1.2	641	1	HS72_DROME	P55063 rattus norv	807	1.2	654	1	HS77_YEAST	P12398 saccharomyc
735	6	1.2	641	1	HS73_RAT	P22202 saccharomyc	808	1.2	655	1	YCO9_SCHPO	Q13674 schizosacch
736	6	1.2	641	1	HS74_YEAST	P29843 drosophila	809	1.2	655	1	GR78_MOUSE	P20029 mus musculu
737	6	1.2	641	1	HS7A_DROME	P16627 mus musculu	810	1.2	655	1	GR78_PLAFO	Q05866 plasmodium
738	6	1.2	641	1	HS7H_HUMAN	P48205 francisella	811	1.2	655	1	HS70_DAUCA	P26791 daucus caro
739	6	1.2	641	1	DNAX_FRATU	Q9jvq9 neisseria m	812	1.2	655	1	HS71_CANAL	P41797 candida alb
740	6	1.2	642	1	DNAX_NEIMA	Q9k0n4 neisseria m	813	1.2	655	1	TR21_MOUSE	Q9epu5 mus musculu
741	6	1.2	642	1	DNAX_NEIMB	P82910 drosophila	814	1.2	655	1	YS44_CABEL	Q09372 caenorhabdi
742	6	1.2	642	1	HS70_DROME	P53623 pichia angu	815	1.2	656	1	DNAX_ALCEU	O33522 alcaligenes
743	6	1.2	642	1	HS72_PICAN	P27400 simian foam	816	1.2	656	1	DNAX_COXBU	O87712 coxiella bu
744	6	1.2	642	1	GAG_SFV3L	P40918 cladosporiu	817	1.2	656	1	HS71_TRYCR	P20593 trypanosoma
745	6	1.2	643	1	HS70_CLAHE	Q10265 schizosacch	818	1.2	656	1	HS7C_DROME	P29844 drosophila
746	6	1.2	643	1	HS71_DROME	P02825 drosophila	819	1.2	657	1	HS7F_CABEL	P11141 caenorhabdi
747	6	1.2	643	1	HS71_SCHPO	Q13614 homo sapien	820	1.2	658	1	GR78_XENLA	Q91883 xenopus lae
748	6	1.2	643	1	HS76_HUMAN	Q04967 homo sapien	821	1.2	660	1	DNAX_CHLTP	P17821 chlamydia t
749	6	1.2	643	1	HS76_PIG	Q13614 homo sapien	822	1.2	660	1	DNAX_CHLTP	P27542 chlamydia p
750	6	1.2	643	1	MTR2_HUMAN	Q32482 legionella	823	1.2	661	1	DHSA_DROME	Q94523 drosophila
751	6	1.2	644	1	DNAX_LEGPN	O06430 nitrosomona	824	1.2	661	1	HS74_TRYBB	P11145 trypanosoma
752	6	1.2	644	1	DNAX_NITEU	P27541 brugia mala	825	1.2	661	1	HS7C_CABEL	P27420 caenorhabdi
753	6	1.2	644	1	HS70_BRUMA	Q91233 oncorhynch	826	1.2	662	1	GR78_NEUCR	P78695 neurospora
754	6	1.2	644	1	HS70_ONCTS	P53421 pichia angu	827	1.2	662	1	SL51_RABIT	P11170 oryctolagus
755	6	1.2	644	1	HS71_PICAN	P27322 lycopersico	828	1.2	663	1	BIP2_MAIZE	P24067 ze mays (m
756	6	1.2	644	1	HS71_LYCES	P06421 human papil	829	1.2	663	1	BIP3_MATZE	Q24581 ze mays (m
757	6	1.2	644	1	VEI_HPV33	P26543 human papil	830	1.2	663	1	GR78_SCHPO	P36604 schizosacch
758	6	1.2	644	1	YED0_YEAST	P39987 saccharomyc	831	1.2	664	1	DEL1_CABEL	Q19038 caenorhabdi
759	6	1.2	644	1	DNAX_LEPIN	P71442 leptospira	832	1.2	664	1	DHSA_HUMAN	P31040 homo sapien
760	6	1.2	645	1	HS70_MAIZE	P11143 ze mays (m	833	1.2	665	1	DHSA_BOVIN	P53791 ovis aries
761	6	1.2	645	1	HS70_PLEWA	Q91291 pleurodeles	834	1.2	665	1	BIP_LYCES	P31039 bos taurus
762	6	1.2	645	1			835	1.2	666	1		P49118 lycopersico
763	6	1.2	645	1			836	1.2	666	1	POL_FMD	P09523 figwort mos

837	6	1.2	667	1	BIP4_TORAC	Q03684 nicotiana t	910	6	1.2	763	1	RGT2_YEAST	Q12300 saccharomyc
838	6	1.2	667	1	GR78_APLCA	Q16956 alysia cal	911	6	1.2	769	1	HCRA_THAAR	Q33819 thauera aro
839	6	1.2	668	1	BIP2_ARATH	Q39043 arabidopsis	912	6	1.2	771	1	DNK3_SYNY3	P73098 synechocyst
840	6	1.2	668	1	BIP5_TORAC	Q03685 nicotiana t	913	6	1.2	772	1	YICI_ECOLI	P31434 escherichia
841	6	1.2	668	1	BIP5_SPIOL	Q42434 spinacia ol	914	6	1.2	773	1	AD11_MOUSE	Q9rlv4 mus musculus
842	6	1.2	669	1	BIP1_ARATH	Q9lkr3 arabidopsis	915	6	1.2	776	1	SM4F_RAT	Q9rl43 rattus norv
843	6	1.2	669	1	EXL1_MOUSE	Q9jlv7 mus musculus	916	6	1.2	776	1	VP4_ROTTP5	P11114 porcine tot
844	6	1.2	670	1	GR78_YARLI	Q99170 yarrowia li	917	6	1.2	776	1	VP4_ROTTP5	P25174 porcine tot
845	6	1.2	670	1	ILVB_ARATH	Q17597 arabidopsis	918	6	1.2	777	1	SM4F_MOUSE	Q92123 mus musculu
846	6	1.2	670	1	YAYF_SCHPO	Q10222 schizosacch	919	6	1.2	781	1	NANH_VIBCH	P37060 vibrio chol
847	6	1.2	673	1	SM4B_HUMAN	Q22774 schizosacch	920	6	1.2	785	1	CAD7_CHICK	Q90763 gallus gall
848	6	1.2	674	1	HS7M_SCHPO	O87906 bacillus th	921	6	1.2	788	1	REC2_HAEIN	P44408 haemophilus
849	6	1.2	675	1	CPAA_BACTJ	P37900 pisum sativ	922	6	1.2	794	1	YE14_YEAST	P39961 saccharomyc
850	6	1.2	675	1	HS7M_PEA	Q01899 phaseolus v	923	6	1.2	796	1	YH04_YEAST	P39888 saccharomyc
851	6	1.2	676	1	HS7M_PHAVU	Q16394 breimia lact	924	6	1.2	797	1	YGLX_HSVBEB	Q9v5e1 homo sapien
852	6	1.2	676	1	HS70_BRELC	Q35501 cricetus	925	6	1.2	797	1	CADK_HUMAN	P28968 equine herp
853	6	1.2	679	1	GR75_CRIGR	P38647 mus musculu	926	6	1.2	801	1	MUTS_THEAQ	Q9hbt6 homo sapien
854	6	1.2	679	1	GR75_HUMAN	P48721 rattus norv	927	6	1.2	811	1	MUTS_THEAQ	Q56215 thermus aqu
855	6	1.2	679	1	GR75_MOUSE	P22010 kiuyveromyc	928	6	1.2	813	1	PMAX_ARATH	Q9t0e0 arabidopsis
856	6	1.2	679	1	GR75_RAT	Q01899 phaseolus v	929	6	1.2	814	1	CADF_HUMAN	P52911 homo sapien
857	6	1.2	679	1	GR78_KLULA	Q16394 breimia lact	930	6	1.2	815	1	AD15_MOUSE	O88839 mus musculu
858	6	1.2	680	1	HS70_TRYCR	P05456 trypanosoma	931	6	1.2	816	1	AD15_RAT	Q9qv00 r adam 15 p
859	6	1.2	681	1	HS70_PLAFA	P11144 plasmodium	932	6	1.2	816	1	HUNE_DROVI	P13361 drosophila
860	6	1.2	682	1	GR78_YEAST	P16474 saccharomyc	933	6	1.2	817	1	MUTS_YEAST	P53278 saccharomyc
861	6	1.2	682	1	HS7M_SOLITU	Q08276 solanum tub	934	6	1.2	818	1	MUTS_THETH	Q921x6 thermus cal
862	6	1.2	682	1	NPH1_CAEEL	O17972 caenorhabdi	935	6	1.2	819	1	AHM1_ARATH	Q9m3h5 arabidopsis
863	6	1.2	682	1	OR66_NPVOP	O10305 oryza pseu	936	6	1.2	826	1	YK83_CAEEL	Q30609 caenorhabdi
864	6	1.2	682	1	NU5C_SESIN	Q33113 sesamum ind	937	6	1.2	830	1	YK83_CAEEL	P40850 saccharomyc
865	6	1.2	684	1	DL14_HUMAN	Q9nr61 homo sapien	938	6	1.2	833	1	HMDH_AGRIP	Q76819 agrotis ips
866	6	1.2	686	1	HS7C_ORYLA	Q05746 plasmodium	939	6	1.2	839	1	YNE1_YEAST	P45382 haemophilus
867	6	1.2	686	1	HS7C_ORYLA	Q9w6y1 oryza lat	940	6	1.2	855	1	ENV_HVLOY	P39559 saccharomyc
868	6	1.2	687	1	HS7E_DROME	P29845 drosophila	941	6	1.2	862	1	CNRC_CHICK	P20888 human immun
869	6	1.2	688	1	DNK1_ANASP	Q9zej6 anabaena sp	942	6	1.2	862	1	SYV_THETH	P52731 gallus gall
870	6	1.2	688	1	DNK1_ANAVA	O05714 anabaena va	943	6	1.2	868	1	NRG2_RAT	P96142 thermus the
871	6	1.2	688	1	ENV_MMTVB	P10259 mouse mamma	944	6	1.2	868	1	NRG2_RAT	Q35569 rattus norv
872	6	1.2	688	1	ENV_MMTVB	P03374 mouse mamma	945	6	1.2	871	1	NPPI_MOUSE	O35569 rattus norv
873	6	1.2	688	1	TH1B_XENLA	Q91641 xenopus lae	946	6	1.2	871	1	NPPI_MOUSE	P06802 mus musculu
874	6	1.2	690	1	E75_CHOPU	O01639 choristoneu	947	6	1.2	875	1	STY_YERPE	Q82b18 versinia pe
875	6	1.2	690	1	NCPR_YEAST	P16603 saccharomyc	948	6	1.2	880	1	GYRA_HAEIN	P43700 haemophilus
876	6	1.2	692	1	DNK1_SYNY3	Q58154 synechocyst	949	6	1.2	880	1	TRK2_SCHPO	Q10065 schizosacch
877	6	1.2	695	1	HRPI_PSEY	P36655 pseudomonas	950	6	1.2	886	1	ACOC_CAEEL	P55849 mus musculu
878	6	1.2	695	1	NICA_DROME	Q9vc22 drosophila	951	6	1.2	887	1	ACON_LEGPN	Q23500 caenorhabdi
879	6	1.2	699	1	E75_MANSE	Q08893 manduca sex	952	6	1.2	891	1	DSC3_BOVIN	P37032 legionella
880	6	1.2	699	1	M1B1_HUMAN	Q9ukm7 homo sapien	953	6	1.2	896	1	NAH5_HUMAN	Q28060 bos taurus
881	6	1.2	699	1	SRCH_HUMAN	P23327 rattus norv	954	6	1.2	896	1	NAH5_HUMAN	Q14940 homo sapien
882	6	1.2	700	1	LSHR_RAT	P16235 rattus norv	955	6	1.2	898	1	NAH5_RAT	Q920x2 rattus norv
883	6	1.2	701	1	EFG_MICLUJ	P09552 micrococcus	956	6	1.2	898	1	ZO71_XENLA	P18751 xenopus lae
884	6	1.2	701	1	LOXR_HUMAN	O75342 homo sapien	957	6	1.2	902	1	MOPT_ARATH	Q29052 sus scrofa
885	6	1.2	701	1	LOXR_MOUSE	O70582 mus musculu	958	6	1.2	902	1	MOPT_ARATH	P43024 arabidopsis
886	6	1.2	705	1	HS70_AJECA	Q00043 ajellomyces	959	6	1.2	906	1	ACON_BRAJA	P70920 bradyrhizob
887	6	1.2	706	1	HS7S_PEA	Q02028 pisum sativ	960	6	1.2	908	1	ACON_BACSU	P09339 bacillus su
888	6	1.2	707	1	NU5C_MALAR	Q9mv16 malvaviscus	961	6	1.2	916	1	PMAL_AJECA	Q07421 ajellomyces
889	6	1.2	708	1	CA0A_CANMA	P05335 candida mal	962	6	1.2	918	1	PMAL_CAEEL	P34487 caenorhabdi
890	6	1.2	708	1	NICA_MOUSE	P57716 mus musculu	963	6	1.2	919	1	PMAL_SCHPO	P09627 schizosacch
891	6	1.2	709	1	NICA_HUMAN	Q92542 homo sapien	964	6	1.2	923	1	LOXC_ORYSA	P38419 oryza sativ
892	6	1.2	709	1	NU5C_PACAQ	Q9mkk2 pachira aqu	965	6	1.2	925	1	YBK4_YEAST	P38164 saccharomyc
893	6	1.2	710	1	DA_DROME	P11420 drosophila	966	6	1.2	925	1	YBK4_YEAST	Q02328 caenorhabdi
894	6	1.2	711	1	E75_GALME	P50239 gallieria me	967	6	1.2	927	1	YOL3_CAEEL	Q63406 rattus norv
895	6	1.2	711	1	PO22_POPJA	Q03274 popillia ja	968	6	1.2	937	1	DBS_RAT	P39523 saccharomyc
896	6	1.2	713	1	CDG2_PAEMA	P31835 paenibacill	969	6	1.2	943	1	YML1_YEAST	P39523 saccharomyc
897	6	1.2	714	1	CDG1_PAEMA	P04830 paenibacill	970	6	1.2	944	1	GLND_RHILV	Q9rae4 rhizobium l
898	6	1.2	715	1	IGAA_YERPE	P58722 yersinia pe	971	6	1.2	946	1	AMYG_CANAL	Q9rae4 candida alb
899	6	1.2	717	1	EMLI_HUMAN	O00423 homo sapien	972	6	1.2	946	1	CITC_YEAST	P07245 s c-1-tetra
900	6	1.2	722	1	MEPL_TOBAC	Q9m7j4 nicotiana t	973	6	1.2	953	1	GLNE_BCOLI	P07245 s c-1-tetra
901	6	1.2	725	1	MCCA_HUMAN	Q96rq3 homo sapien	974	6	1.2	954	1	DRP2_HUMAN	Q38796 arabidopsis
902	6	1.2	726	1	AMSA_ERWAM	Q46631 erwinia amy	975	6	1.2	955	1	KINL_LEICH	P07245 s c-1-tetra
903	6	1.2	730	1	ELS_HUMAN	P15502 homo sapien	976	6	1.2	961	1	GBR1_MOUSE	Q38796 arabidopsis
904	6	1.2	732	1	CADL_CHICK	P33145 gallus gall	977	6	1.2	961	1	ACON_MYCAV	Q08451 mycobacteri
905	6	1.2	736	1	NTT5_HUMAN	Q9gznb homo sapien	978	6	1.2	961	1	GBR1_HUMAN	Q9u85 homo sapien
906	6	1.2	737	1	CATA_YERPE	Q9xgb0 yersinia pe	979	6	1.2	967	1	ATSI1_HUMAN	Q9u85 homo sapien
907	6	1.2	749	1	DNK3_SYNP7	P50022 synechococ	980	6	1.2	967	1	ATSI1_RAT	Q9u85 homo sapien
908	6	1.2	750	1	NU5C_TECST	Q9tlc2 tecoma stan	981	6	1.2	968	1	ATSI1_MOUSE	Q9u85 homo sapien
909	6	1.2	758	1	PURL_CORAM	Q9rhw9 corynebacte	982	6	1.2	968	1	ATSI1_MOUSE	P97857 mus musculu

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983 6 1.2 975 1 CLTM_YEAST
984 6 1.2 991 1 GBRL_RAT
985 6 1.2 994 1 SVL_XYLEFA
986 6 1.2 1007 1 CHC2_HUMAN
987 6 1.2 1014 1 EPB6_MOUSE
988 6 1.2 1015 1 FONG_ECOLI
989 6 1.2 1015 1 YRD3_DROME
990 6 1.2 1020 1 YRD3_DROME
991 6 1.2 1025 1 PO21_NAUVI
992 6 1.2 1026 1 DHE2_NEUCR
993 6 1.2 1030 1 STK9_HUMAN
994 6 1.2 1030 1 VPK1_CAEEL
995 6 1.2 1038 1 BMR2_HUMAN
996 6 1.2 1038 1 BMR2_MOUSE
997 6 1.2 1042 1 ATHL_BUFMA
998 6 1.2 1043 1 DSG1_BOVIN
999 6 1.2 1044 1 ITA8_CHICK
1000 6 1.2 1046 1 K052_HUMAN

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ALIGNMENTS

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RESULT 1
ID ARSB_STA0U STANDARD; PRT; 429 AA.
AC P30329;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Arsenical pump membrane protein.
GN ARSB.
OS Staphylococcus aureus.
OC Plasmid p1258.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92276351; PubMed=1534328;
RA Ji G., Silver S.;
RT "Regulation and expression of the arsenic resistance operon from
RT Staphylococcus aureus plasmid p1258.";
RL J. Bacteriol. 174:3684-3694(1992).
CC -!- FUNCTION: INVOLVED IN ARSENICAL RESISTANCE. THOUGHT TO FORM THE
CC CHANNEL OF AN ARSENITE PUMP.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -----
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CC -----
CC EMBL; M86824; AAA25637.1; -
CC PIR; C41903;
CC InterPro; IPR000802; Ars_pump.
CC Pfam; PF02040; ARSB; 1.
CC PRINTS; PR00758; ARSENICPUMP.
CC TIGRFS; TIGR00935; 2a45; 1.
CC Plasmid; Arsenical resistance; Transmembrane.
CC SEQUENCE 429 AA; 46484 MW; 654CE9BA110A15DB CRC64;

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```

Query Match 1.6%; Score 8; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 430 IVLAVLLV 437
DB 230 IVLAVLLV 237

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RESULT 2
VES_HPV33 STANDARD; PRT; 75 AA.
ID VES_HPV33
AC P06426;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Probable E5 protein.
GN E5.
OS Human papillomavirus type 33.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10586;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86200464; PubMed=3009902;
RA Cole S.T., Streeck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus
RT type 33, which is associated with cervical cancer.";
RL J. Virol. 58:991-995(1986).
CC -----
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CC -----
CC EMBL; M12732; AAA46962.1; -
CC PIR; A03679; W5WL33.
CC InterPro; IPR004270; Papilloma_E5.
CC Pfam; PF03025; Papilloma_E5; 1.
CC Early protein.
CC SEQUENCE 75 AA; 8906 MW; CDC414CA37052CA8 CRC64;

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Query Match 1.4%; Score 7; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 WLLVLVL 12
DB 31 WLLVLVL 37

```

```

RESULT 3
VES_HPV58 STANDARD; PRT; 76 AA.
ID VES_HPV58
AC Z26552;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Probable E5 protein.
GN E5.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92024102; PubMed=1656594;
RA Kirii Y., Iwamoto S., Matsukura T.;
RT "Human papillomavirus type 58 DNA sequence.";
RL Virology 185:424-427(1991).
CC -----
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CC -----
CC EMBL; M86824; AAA25637.1; -
CC PIR; C41903;
CC InterPro; IPR000802; Ars_pump.
CC Pfam; PF02040; ARSB; 1.
CC PRINTS; PR00758; ARSENICPUMP.
CC TIGRFS; TIGR00935; 2a45; 1.
CC Plasmid; Arsenical resistance; Transmembrane.
CC SEQUENCE 429 AA; 46484 MW; 654CE9BA110A15DB CRC64;

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Wed Apr 23 07:41:52 2003

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DR EMBL; D90400; BAA31849.1; -.
DR PIR; D36779; W5WL58.
DR InterPro; IPR004270; Papilloma_E5.
DR Pfam; PF03025; Papilloma_E5; 1.
KW Early protein.
SQ SEQUENCE 76 AA; 8953 MW; C4B6E29BC1D5BA76 CRC64;
Query Match 1.4%; Score 7; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 WLLVVL 12
DB 32 WLLVVL 38
RESULT 4
VG9_SpVIR STANDARD; PRT; 78 AA.
AC PL5900;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Gene 9 protein.
GN 9.
OS Spiroplasma virus SpV1-R8A2 B.
OC Viruses; ssDNA viruses; Inoviridae; Plectrovirus.
ON NCBI_TaxID=10854;
RX MEDLINE=90206799; PubMed=2320423;
RA Renaudin J., Aulio P., Vignault J.C., Bove J.M.;
RT "Complete nucleotide sequence of the genome of Spiroplasma citri
RL Nucleic Acids Res. 18:1293-1293(1990).
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DR EMBL; X51344; CAA35727.1; -.
DR PIR; J01248; JQ1248.
DR InterPro; IPR001896; Plant_vir_prot.
DR Pfam; PF01307; Plant_vir_prot; 1.
DR ProDom; PD001561; Plant_vir_prot; 1.
KW Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 72 92 POTENTIAL.
SQ SEQUENCE 106 AA; 11435 MW; B3366CFBB40C92D6 CRC64;
Query Match 1.4%; Score 7; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 434 VLLVAAI 440
DB 12 VLLVAAI 18
RESULT 6
GALP_PIG STANDARD; PRT; 120 AA.
ID GALP_PIG
AC Q9T95;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Galanin-like peptide precursor.
GN GALP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
ON NCBI_TaxID=9823;
RX MEDLINE=20069685; PubMed=10601261;
RA Ohtaki T., Kumano S., Ishibashi Y., Ogi K., Matsui H., Harada M.,
RA Kitada C., Kurokawa T., Onda H., Fujino M.;
RT "Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
RL J. Biol. Chem. 274:37041-37045(1999).
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DR EMBL; AF188490; AAF19722.1; -.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 22
FT PEPTIDE 23 82
FT PROPEP 85 120
GALANIN-LIKE PEPTIDE.

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SQ SEQUENCE 120 AA; 12681 MW; 709F7D8F42149054 CRC64;
Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 120;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 430 IVLAVILL 436
|||||
DB 8 IVLAVILL 14

RESULT 7
VME1_IBV6
ID VME1_IBV6 STANDARD; PRT; 225 AA.
AC P05136;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
GN M.
OS Avian infectious bronchitis virus (strain 6/82) (IBV).
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11121;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86286562; PubMed=3016650;
RA Binns M.M., Boursnell M.E.G., Tomley F.M., Brown T.D.K.;
RT "Nucleotide sequence encoding the membrane protein of the IBV strain 6/82.";
RL Nucleic Acids Res. 14:5558-5558(1986).
CC -!- FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MAY BE IMPLICATED IN VIRAL PATHOGENESIS.
CC -!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE CORONAVIRUS M PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; X04107; CAA27727.1; -
DR EMBL; D00005; BAA00003.1; -
DR PIR; A23649; MTH68.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
KW Matrix protein; Transmembrane; Glycoprotein.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 47 67 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
SQ SEQUENCE 225 AA; 25465 MW; AF46122BFFC2EF7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 225;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 436 LVAAIIL 442
|||||
DB 79 LVAAIIL 85

RESULT 8
VME1_IBV6
ID VME1_IBV6 STANDARD; PRT; 225 AA.
AC P04327;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
GN M.
OS Avian infectious bronchitis virus (strain Beaudette M42) (IBV).
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11123;
RN [1]
RP SEQUENCE.
RX MEDLINE=88007845; PubMed=2821010;
RA Machamer C.E., Rose J.K.;
RT "A specific transmembrane domain of a coronavirus E1 glycoprotein is required for its retention in the Golgi region.";
RL J. Cell Biol. 105:1205-1214(1987).
CC -!- FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MAY BE IMPLICATED IN VIRAL PATHOGENESIS.
CC -!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE CORONAVIRUS M PROTEIN FAMILY.
CC -----
DR EMBL; M95169; AAA70239.1; -
DR EMBL; M22014; AAA46215.1; -
DR PIR; A04022; MTHIV.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
KW Matrix protein; Transmembrane; Glycoprotein.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 47 67 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
SQ SEQUENCE 225 AA; 25475 MW; D5AE8685CF78220D CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 225;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 436 LVAAIIL 442
|||||
DB 79 LVAAIIL 85

RESULT 9
VME1_IBV6
ID VME1_IBV6 STANDARD; PRT; 225 AA.
AC P11222;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
GN M.
OS Avian infectious bronchitis virus (strain Beaudette M42) (IBV).
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11123;
RN [1]
RP SEQUENCE.
RX MEDLINE=88007845; PubMed=2821010;
RA Machamer C.E., Rose J.K.;
RT "A specific transmembrane domain of a coronavirus E1 glycoprotein is required for its retention in the Golgi region.";
RL J. Cell Biol. 105:1205-1214(1987).
CC -!- FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MAY BE IMPLICATED IN VIRAL PATHOGENESIS.
CC -!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE CORONAVIRUS M PROTEIN FAMILY.
CC -----
DR EMBL; M95169; AAA70239.1; -
DR EMBL; M22014; AAA46215.1; -
DR PIR; A04022; MTHIV.
DR InterPro; IPR002574; Corona_M.
DR Pfam; PF01635; Corona_M.1.
KW Matrix protein; Transmembrane; Glycoprotein.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT TRANSMEM 47 67 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
SQ SEQUENCE 225 AA; 25475 MW; D5AE8685CF78220D CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 225;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 436 LVAAIIL 442
|||||
DB 79 LVAAIIL 85

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DR Pfam: PF01635; Corona_M; 1.
 KW Matrix protein; Transmembrane; Glycoprotein.
 FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .).
 FT TRANSMEM 21 42 POTENTIAL.
 FT TRANSMEM 52 72 POTENTIAL.
 FT TRANSMEM 78 101 POTENTIAL.
 SQ SEQUENCE 225 AA; 25477 MW; 466349883C7B2D21 CRC64;

Query Match 1.4%; Score 7; DB 1; Length 225;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 436 LVAAIIL 442
 | | | | |
 Db 79 LVAAIIL 85

RESULT 10
 VMEI_IBVK
 ID VMEI_IBVK STANDARD; PRT; 225 AA.
 AC P12649;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE E1 glycoprotein (Matrix glycoprotein) (Membrane glycoprotein).
 GN M.
 OS Avian infectious bronchitis virus (strain KB523) (IBV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OX NCBI_TaxID=11126;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88306251; PubMed=2841803;
 RA Sutou S., Sato S., Okabe T., Nakai M., Sasaki N.;
 RT "Cloning and sequencing of genes encoding structural proteins of
 RT avian infectious bronchitis virus";
 RL Virology 165:589-595(1988).
 CC -!- FUNCTION: TARGETS THE SITE OF VIRUS MORPHOGENESIS AND MAY BE
 CC IMPLICATED IN VIRAL PATHOGENESIS.
 CC -!- SUBCELLULAR LOCATION: LARGELY EMBEDDED IN THE LIPID BILAYER.
 CC -!- SIMILARITY: BELONGS TO THE CORONAVIRUS M PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; M21515; AAA6581.1; -
 DR PIR; C29249; MNIHAI.
 DR InterPro; IPR002574; Corona_M.
 DR Pfam; PF01635; Corona_M; 1.
 KW Matrix protein; Transmembrane; Glycoprotein.
 FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT TRANSMEM 21 41 POTENTIAL.
 FT TRANSMEM 47 67 POTENTIAL.
 FT TRANSMEM 78 98 POTENTIAL.
 SQ SEQUENCE 225 AA; 25541 MW; F76DA96A71416932 CRC64;

Query Match 1.4%; Score 7; DB 1; Length 225;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 436 LVAAIIL 442
 | | | | |
 Db 79 LVAAIIL 85

RESULT 11

VGI6_BPPHC
 ID VGI6_BPPHC STANDARD; PRT; 237 AA.
 AC Q9ZX92;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Gene 16 protein (GP16).
 GN 16.
 OS Bacteriophage phi-C31.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC Lambda-like viruses.
 OX NCBI_TaxID=10719;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Norwich Stock;
 RX MEDLINE=99162580; PubMed=10051617;
 RA Hendrix R.W., Smith M.C.M., Burns N., Ford M.E., Hatfull G.F.;
 RT "Evolutionary relationships among diverse bacteriophages and
 RT prophages: all the world's a phage";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:2192-2197(1999).
 CC -!- SIMILARITY: BELONGS TO THE THY1 FAMILY
 CC -----
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 CC -----
 CC EMBL; AJ006589; CAA07140.1; -
 DR InterPro; IPR003669; Thyl.
 DR Pfam; PF02511; Thyl; 1.
 SQ SEQUENCE 237 AA; 26016 MW; 3FDEF9BA6DF302C0 CRC64;

Query Match 1.4%; Score 7; DB 1; Length 237;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 REAARAL 19
 | | | | |
 Db 165 REAARAL 171

RESULT 12
 YCXE_BACME
 ID YCXE_BACME STANDARD; PRT; 286 AA.
 AC P40419;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 30.5 kDa protein in gdh1 5' region (ORF 2).
 OS Bacillus megaterium.
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1404;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IAM 1030;
 RA Mitamura T., Ebara R.V., Nakai T., Makino Y., Negoro S., Urabe I.,
 RA Okada H.;
 RT "Structure of isozyme genes of glucose dehydrogenase from Bacillus
 RT megaterium IAM1030";
 RL J. Ferment. Bioeng. 70:363-369(1990).
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING SPOULATION.
 CC -!- SIMILARITY: TO A SIMILAR ORF IN B.SUBTILIS.
 CC -----
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 CC -----

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CC -----
DR EMBL; D90043; BAAL4098.1; -
DR PIR; JS0384;
DR InterPro; IPR000620; DUF6.
DR InterPro; IPR004673; RhaT.
DR Pfam; PF00892; DUF6; 1.
DR TIGRfams; TIGR00776; RhaT; 1.
KW Hypothetical protein; Sporulation.
SQ SEQUENCE 286 AA; 30490 MW; 95AB89D02511D74D CRC64;

Query Match 1.4%; Score 7; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 IVGIVLA 433
DB 127 IVGIVLA 133

RESULT 13
V084_HSV6U
ID V084_HSV6U STANDARD; PRT; 342 AA.
AC P52532;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein U84.
GN "Human EDLF2.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10370;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95027704; PubMed=7941342;
RA Nicholas J.;
RT "Nucleotide sequence analysis of a 21-kbp region of the genome of
RT human herpesvirus-6 containing homologues of human cytomegalovirus
RT major immediate-early and replication genes.";
RT Virology 204:738-750(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95266321; PubMed=7747482;
RA Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RA Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content,
RT and genome evolution.";
RL Virology 209:29-51(1995).
CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND
CC HSV-7 U84 AND HCMV UL117.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U13194; AAA68475.1; -
DR EMBL; X83413; CAA58333.1; -
SQ SEQUENCE 342 AA; 39555 MW; 2AF4C6BDEC729C74 CRC64;

Query Match 1.4%; Score 7; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 409 LQNNLSP 415
DB 46 LQNNLSP 52

RESULT 14

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INVE_SALTY
ID INVE_SALTY STANDARD; PRT; 372 AA.
AC P35671;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Invasion protein invE.
GN INVE OR STM2897.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SR11 / SL1344;
RX MEDLINE=92335220; PubMed=1631083;
RA Ginocchio C., Pace J., Galan J.E.;
RT "Identification and molecular characterization of a Salmonella
RT typhimurium gene involved in triggering the internalization of
RT salmonellae into cultured epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:5976-5980(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RN [3]
RP Nature 413:852-856(2001).
RX SEQUENCE OF 1-69 FROM N.A.
RP STRAIN=SR-11;
RX MEDLINE=95089692; PubMed=7997169;
RA Kaniga K., Bossio J.C., Galan J.E.;
RT "The Salmonella typhimurium invasion genes invF and invG encode
RT homologues of the AraC and Pvd family of proteins.";
RL Mol. Microbiol. 13:555-568(1994).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RX STRAIN=TM1;
RX MEDLINE=95172719; PubMed=7868245;
RA Lodge J., Douce G.R., Amin I.I., Bolton A.J., Martin G.D.,
RA Chatfield S., Dougan G., Brown N.L., Stephen J.;
RT "Biological and genetic characterization of TnpA mutants of
RT Salmonella typhimurium TML in the context of gastroenteritis.";
RL Infect. Immun. 63:762-769(1995).
CC -!- FUNCTION: INVOLVED IN THE TRIGGERING OF INTRACELLULAR EVENTS THAT
CC LEAD TO MICROBIAL INTERNALIZATION OF THE INTESTINAL EPITHELIUM.
CC THESE EVENTS INCLUDE INCREASE IN CALCIUM LEVEL, REDISTRIBUTION OF
CC ACTIN MICROFILAMENTS, AND CHANGES IN THE NORMAL STRUCTURE OF THE
CC MICROVILLI.
CC -!- SIMILARITY: TO YERSINIA OUTER MEMBRANE PROTEIN YOPN (LCRE).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M90714; -; NOT_ANNOTATED_CDS.
DR EMBL; AE008832; AAL21777.1; -
DR EMBL; U08280; AAA74041.1; -
DR EMBL; X75302; CAA53050.2; -
DR StyGene; SG10187; invE.
DR InterPro; IPR003520; Invas_invE.
DR Pfam; PF02523; Inve; 1.
KW Virulence; Complete proteome.

```


FT CONFLICT 64 64 Q -> E (IN REF. 1 AND 3).
 FT CONFLICT 117 117 S -> T (IN REF. 1).
 SQ SEQUENCE 372 AA; 42421 MW; 7E10B570D2AF644F CRC64;

Query Match 1.4%; Score 7; DB 1; Length 372;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LVLVLR 14
 DB 125 LVLVLR 131

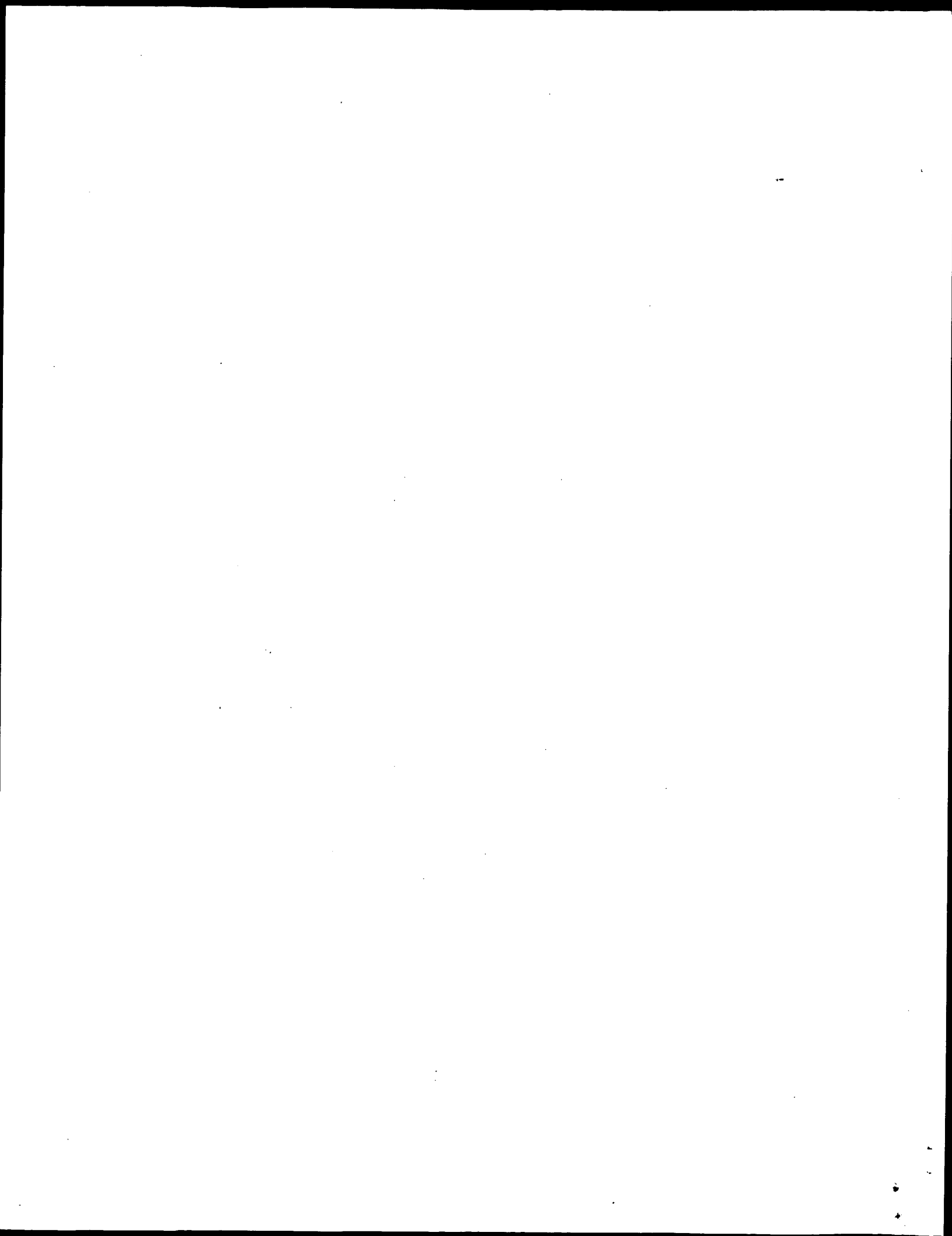
RESULT 15

FTSW_HELPJ STANDARD; PRT; 388 AA.
 AC Q92J48;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable cell division protein ftsw.
 GN FTSW OR JHP1468.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
 CC -!- FUNCTION: THIS IS A SEPTUM-PEPTIDOGLYCAN BIOSYNTHETIC PROTEIN,
 CC INVOLVED IN CELL WALL FORMATION. PLAYS A ROLE IN THE STABILIZATION
 CC OF THE FTSZ RING DURING CELL DIVISION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE FTSW/RODA/SPOVE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AE001568; AAD07042.1; -;
 CC InterPro; IPR001182; Cell-cycle.
 CC Pfam; PF01098; FTSW_RODA_SPOVE; 1.
 CC PROSITE; PS00428; FTSW_RODA_SPOVE; 1.
 CC Peptidoglycan synthesis; Cell wall; Cell division; Cell shape;
 CC Transmembrane; Inner membrane; Complete proteome.
 FT TRANSMEM 7 27 POTENTIAL.
 FT TRANSMEM 39 59 POTENTIAL.
 FT TRANSMEM 71 91 POTENTIAL.
 FT TRANSMEM 106 126 POTENTIAL.
 FT TRANSMEM 145 165 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT TRANSMEM 262 282 POTENTIAL.
 FT TRANSMEM 295 315 POTENTIAL.
 FT TRANSMEM 328 348 POTENTIAL.
 FT TRANSMEM 359 379 POTENTIAL.
 SQ SEQUENCE 388 AA; 42540 MW; 51E4277A910B286D CRC64;

Query Match 1.4%; Score 7; DB 1; Length 388;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 431 VLAVLLV 437
 DB 178 VLAVLLV 184

Search completed: April 22, 2003, 16:17:04
 Job time : 32 secs



GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:03:25 ; Search time 34 Seconds
(without alignments)
3030.105 Million cell updates/sec

Title: US-09-918-715-230
Perfect score: 2691
Sequence: 1 MRCELWLLVLRARALS.....YAEVPSGHEKSGFMEAEQC 500

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2691	100.0	500	4	Q9HCT9		Q9hct9 homo sapien
2	2209	82.1	500	11	Q91ZV7		Q91zv7 mus musculu
3	2203	81.9	500	11	Q9CWV5		Q9cwv5 mus musculu
4	1295	48.1	529	4	Q96PD9		Q96pd9 homo sapien
5	1275.5	47.4	530	11	Q9DC11		Q9dc11 mus musculu
6	1275.5	47.4	530	11	Q91ZV6		Q91zv6 mus musculu
7	1127.5	41.9	480	4	Q96E59		Q96e59 homo sapien
8	660.5	24.5	625	5	Q9WZV9		Q9wzv9 drosophila
9	611	22.7	476	5	Q18500		Q18500 caenorhabdi
10	297.5	11.1	151	4	Q96S09		Q96su9 homo sapien
11	126	4.7	1161	5	Q04901		Q04901 halocynthia
12	117	4.3	308	4	Q9UN94		Q9un94 homo sapien
13	115.5	4.3	1568	4	O60486		O60486 homo sapien
14	111.5	4.1	366	4	Q9UN95		Q9un95 homo sapien
15	111.5	4.1	877	4	Q9H3Q6		Q9h3q6 homo sapien
16	111.5	4.1	878	4	Q9H3Q7		Q9h3q7 homo sapien

Q9ukw9 homo sapien
Q9hl95 homo sapien
Q9gz22 homo sapien
Q9fl73 streptococ
Q9fb48 corynebacte
Q9fv73 arabidopsis
Q9r4u3 mus musculu
Q9ly36 mus musculu
O68868 synechococ
O54916 mus musculu
Q9fls3 streptococ
Q9yly7 ephydatia f
Q9lmn7 arabidopsis
Q96d71 homo sapien
Q9bxy9 homo sapien
Q9gta4 leishmania
Q9r4u4 rattus norv
Q9av18 oryza sativ
Q8tbd9 homo sapien
Q9ug37 homo sapien
Q9hcal homo sapien
Q9v4b6 homo sapien
Q13446 caenorhabdi
Q9sxx8 nicotiana t
P90662 aedes aegypt
Q9flj8 arabidopsis
Q9qzc2 mus musculu
O08758 mus musculu
O57106 inkoo virus

ALIGNMENTS

RESULT 1

Q9HCT9 PRELIMINARY; PRT; 500 AA.
ID Q9HCT9;
AC Q9HCT9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor endothelial marker 7 precursor (Tumor endothelial marker 3 precursor).
DE precursor).
GN TEM7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20407466; PubMed=10947988;
RA St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,
RA Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein B.,
RA Kinzler K.W.;
RT "Genes expressed in human tumor endothelium."
RL Science 289:1197-1202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA St Croix B., Vogelstein B., Kinzler K.W.;
RN Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carlson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and humans."
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF279144; AAC00869.2; -;
DR EMBL; AF378753; AAL11990.1; -;
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR002165; Flexin_repeat.
DR InterPro; IPR003975; Shal_channel.

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR ENBL: AK010361; BAB26881.1; -;
 DR MGD: MGI:1919574; 2410003107Rik.
 DR InterPro: IPR003886; Nidogen_ext.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR002165; Plexin-repeat.
 DR Pfam: PF01437; PSI: 1.
 DR SMART: SM00539; NIDO: 1.
 DR SMART: SM00423; PSI: 1.
 SQ SEQUENCE 500 AA; 55635 MW; 802D6865F8CA18BD CRC64;
 Query Match 81.9%; Score 2203; DB 11; Length 500;
 Best Local Similarity 81.4%; Pred. No. 2.1e-188;
 Matches 408; Conservative 46; Mismatches 45; Indels 2; Gaps 2;
 QY 1 MRGELWLL-VLVREARALSPQAGHDEGPGSGAAKGTVRGNNRRARESPGHVSEPD 59
 DB 1 MRAQLWLLQLLLRGAALSPATPAGHNEQGSAAWAKTRQGSRRPRSPAQVLKPG 60
 QY 60 RTQLSODLGGTGLAMDTLPDNRTRVEDNHSYVSRLYGSEPHSRELWVDVAEANKSQV 119
 DB 61 KTQLSODLGGSLAIDTLPDNRTRVEDNHNYSYVSRVYGPCKSQSLDWDLAVANRSHV 120
 QY 120 KHTILSNTHRQASRVLSDFPFYGHPLRQITATGGTFPMGDVIRHMLTATQYVAPLM 179
 DB 121 KIHRLSSSRHQASRVLSDFPFYGHPLRQITATGGTFPMGDVIRHMLTATQYVAPLM 180
 QY 180 ANFNPGYSDNSTVYFDNGTVFVQWQDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIP 239
 DB 181 ANFNPGYSDNSTVYFDNGTVFVQWQDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIP 240
 QY 240 MSVPISISSQHPVKTKGLSDAFMILNPSDPVPESRRRSIFEFYHRIELDPKSVTSMSAVEFT 299
 DB 241 MAVLDISSAHPVKAGLSDAFMILNPSDEVPASQRRTIFEFYHVELDSSKITTTSAVEFT 300
 QY 300 PLPTCLQHRSCDACHSSDLTFNCSCWCHVLRCSGFDYRQEWMDYCAQAEAGRMCDGF 359
 DB 301 PLPTCLQHRSCDACHSSDLTFNCSCWCHVLRCSGFDYRQEWMDYCAQAEAGRMCDGF 360
 QY 360 QDEHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNPAAGDGLQNNLSPKTKG 419
 DB 361 QDHSYASPDTSFSPFNGD-STTSSSLFIDSLTTEDDTKLNPAAGDGLPDHSPKSG 419
 QY 420 TPVHLGTIVGIVLVAIIAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSH 479
 DB 420 TPVHLGTIVGIVLVAIIAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSH 479
 QY 480 TYAEVPSGHEKEGFEAEQC 500
 DB 480 TYAEVPSGHEKEGFEAEQC 500
 RESULT 4
 Q96PD9 PRELIMINARY; PRT; 529 AA.
 AC Q96PD9; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Tumor endothelial marker 7-related precursor.
 GN TEM7R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21443268; PubMed=11559528;
 RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
 RA Kinzler K.W., St Croix B.,
 RT "Cell surface tumor endothelial markers are conserved in mice and humans."
 RL Cancer Res. 61:6649-6655(2001).
 DR EMBL: AF378757; AAL11994.1; -;
 DR InterPro: IPR002165; Plexin-repeat.
 DR Pfam: PF01437; PSI: 1.
 KW SIGNAL.
 FT CHAIN 1 30 POTENTIAL.
 FT CHAIN 31 529 TUMOR ENDOTHELIAL MARKER 7-RELATED.
 SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;
 Query Match 48.1%; Score 1295; DB 4; Length 529;
 Best Local Similarity 57.3%; Pred. No. 3.9e-107;
 Matches 250; Conservative 72; Mismatches 106; Indels 8; Gaps 5;
 QY 72 LAMDTLPDNRTRVED-NHSYVSRLYGSEPHSRELWVDVAEANKRSQVKIHTILSNTHR 130
 DB 95 LLLDDGQDNTQTEEDTDHNYISRIYGPSDSASDLWVNDIDMEKDKVHIGILSNTHR 154
 QY 131 QASRVLSDFPFYGHPLRQITATGGTFPMGDVIRHMLTATQYVAPLMANFNPGYSDNS 190
 DB 155 QAARVNSLDFPFYGHPLRQITATGGTFYGEVHRLTATQYIAPLMANFDPSPVSRNS 214
 QY 191 TVYFDNGTVFVQWQDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPMSVPEISSOH 250
 DB 215 TVYFDNGTVFVQWQDHVYLGQWEDKGSFTFOAALHHDGRIVFAYKEIPVLTQISSTNH 274
 QY 251 PVKTKGLSDAFMILNPSDPVPESRRRSIFEFYHRIELDPKSVTSMSAVEFTPLPTCLQHRSC 310
 DB 275 PVKTKGLSDAFMILNPSDPVPESRRRSIFEFYHRIELDPKSVTSMSAVEFTPLPTCLQHRSC 334
 QY 311 DACWSSDLTFNCSCWCHVLRCSGFDYRQEWMDYCAQAEAGRMCDGFQDEHDSASPD 370
 DB 335 GPCVSSQIGFNCSCWCHVLRCSGFDYRQEWMDYCAQAEAGRMCDGFQDEHDSASPD 394
 QY 371 T-SFSPYDGLTTTSSSLFIDSLTTEDDTKLNPAAGDGLQ-NNLSPKTKGTPVHL 424
 DB 395 TIGATTTFQFVLTTRAVTSQFPTSLPTEDDTKIALHLKDNAGSTDDSAEAKGGLHA 454
 QY 425 GTIVGIVLVAIIAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHSH 484
 DB 455 GLVIGLILVIVATILVTVYVYHPTSAASIFFIERRPSPWPAKFRSGHGPAYAEV 514
 QY 485 EPSGHEKEGFEAEQC 500
 DB 515 EPVG-EKEGFEVSEQC 529
 RESULT 5
 Q9DC11 PRELIMINARY; PRT; 530 AA.
 AC Q9DC11; 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE 1200007L24RIK protein.
 GN 1200007L24RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=LUNG;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Koichiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombeerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Yushanaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection.;
 RL Nature 409:685-690(2001).
 DR EMBL: AK004640; BAB23431.1; -;
 DR MGD: MGI:1914698; 1200007L24Rik.
 DR InterPro: IPR003886; Nidogen_ext.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR002165; plexin_repeat.
 DR Pfam: PF01437; PSI: 1.
 DR SMART: SM00539; NIDO: 1.
 DR SMART: SM00423; PSI: 1.
 SQ SEQUENCE 530 AA; 59616 MW; FB956C020735E36D CRC64;

Query Match 47.4%; Score 1275.5; DB 11; Length 530;
 Best Local Similarity 52.9%; Pred. No. 2.2e-105;
 Matches 248; Conservative 77; Mismatches 129; Indels 15; Gaps 7;

QY 44 WNRARESPGHVSEPDRTQLSQ-----DLGGGTLMADTLPDNRTRVED-NHSYVVSRLYG 98
 Db WKRN--DPFKAVDTNRASMGQASPEKGTDLDDGQDNNTQIEDTDHNYISRIY 122
 QY 99 PSEPHSRELWVDVAEANRSOVKIHILSNTHROASRVLSDFPFYGHPLQIATGGF 158
 Db PADSASRLWVNDOMEKDKVKGILSNTHROARVNLSDFFPYGHFLNEVTVATGGF 182
 QY 159 IFMGDVTHRLMTATQYVAPLMAFNPGYSDNSTVYVFDNGTVFVQWHDVYLOGWEDKGS 218
 Db 183 IYTGVEVHRLMTATQYIAPLMAFNPDPSVSRNSTVRYFDNGTALVQWHDVHLQDNYNLGS 242
 QY 219 FTFOAALHHDGRIVFAYKEIPMSVPEISSOHVPKVTGLSDAFMLNFPDVPESRRSIF 278
 Db 243 FTFOATLLMDGRILFYKEIPVLTQISSTNHPVKVGLSDAFVYVHRIQIIPNVRRRTIY 302
 QY 279 EYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSDLTFNCSWCHVLRQCSGFDY 338
 Db 303 EYHVELQMSKITNISAVEMTPLTCLQFNGCGPCVSSQIGFNCWSKLRQCSGFDH 362
 QY 339 ROEMWDYCAQAEAG--RMCEDFQDEHDSASPTSFSPYDGLTTS-----SSLFIDSL 392
 Db 363 RQWVDSCGPEEVQSKMKCEKTEPGETSQTTSHTTMOFRVLTTRRAVTSQMPSTL 422
 QY 393 TTEDDTKLNYPAGGDLQ--NLSPKTKGTPVHLGTIVGLVAVLLVAAILAGIYINGHP 451
 Db 423 PTEDDTKIALHLKDSGASTDSDSAEKKGGTLAGLIVGLILVLIITAAAILVTYVYVHHP 482
 QY 452 TSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEGFMARQC 500
 Db 483 TSAASIFFIERRPWRPAMKFRSGHPAYAEVPGV-EKEGFIVSEQ 530

RESULT 6

Q912V6 PRELIMINARY; PRT; 530 AA.
 AC Q912V6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Tumor endothelial marker 7-related precursor.
 GN 1200007L24RIK OR TEM7R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21443268; PubMed-11559528;
 RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
 RA Kinzler K.W., St Croix B.;
 RT "Cell surface tumor endothelial markers are conserved in mice and humans."
 RL Cancer Res. 61:6649-6655(2001).
 DR EMBL: AF378761; AALL1198.1; -;
 DR MGD: MGI:1914698; 1200007L24Rik.
 DR InterPro: IPR002165; Plexin_repeat.
 DR Pfam: PF01437; PSI: 1.
 KW SIGNAL.
 FT CHAIN 1 30 POTENTIAL.
 FT CHAIN 31 530 TUMOR ENDOTHELIAL MARKER 7-RELATED.
 SQ SEQUENCE 530 AA; 59625 MW; FF8315020735E36D CRC64;

Query Match 47.4%; Score 1275.5; DB 11; Length 530;
 Best Local Similarity 52.9%; Pred. No. 2.2e-105;
 Matches 248; Conservative 77; Mismatches 129; Indels 15; Gaps 7;

QY 44 WNRARESPGHVSEPDRTQLSQ-----DLGGGTLMADTLPDNRTRVED-NHSYVVSRLYG 98
 Db WKRN--DPFKAVDTNRASMGQASPEKGTDLDDGQDNNTQIEDTDHNYISRIY 122
 QY 99 PSEPHSRELWVDVAEANRSOVKIHILSNTHROASRVLSDFPFYGHPLQIATGGF 158
 Db PADSASRLWVNDOMEKDKVKGILSNTHROARVNLSDFFPYGHFLNEVTVATGGF 182
 QY 159 IFMGDVTHRLMTATQYVAPLMAFNPGYSDNSTVYVFDNGTVFVQWHDVYLOGWEDKGS 218
 Db 183 IYTGVEVHRLMTATQYIAPLMAFNPDPSVSRNSTVRYFDNGTALVQWHDVHLQDNYNLGS 242
 QY 219 FTFOAALHHDGRIVFAYKEIPMSVPEISSOHVPKVTGLSDAFMLNFPDVPESRRSIF 278
 Db 243 FTFOATLLMDGRILFYKEIPVLTQISSTNHPVKVGLSDAFVYVHRIQIIPNVRRRTIY 302
 QY 279 EYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSDLTFNCSWCHVLRQCSGFDY 338
 Db 303 EYHVELQMSKITNISAVEMTPLTCLQFNGCGPCVSSQIGFNCWSKLRQCSGFDH 362
 QY 339 ROEMWDYCAQAEAG--RMCEDFQDEHDSASPTSFSPYDGLTTS-----SSLFIDSL 392
 Db 363 RQWVDSCGPEEVQSKMKCEKTEPGETSQTTSHTTMOFRVLTTRRAVTSQMPSTL 422
 QY 393 TTEDDTKLNYPAGGDLQ--NLSPKTKGTPVHLGTIVGLVAVLLVAAILAGIYINGHP 451
 Db 423 PTEDDTKIALHLKDSGASTDSDSAEKKGGTLAGLIVGLILVLIITAAAILVTYVYVHHP 482
 QY 452 TSNAALFFIERRPHHPAMKFRSHPDHSTYAEVPSGHEKEGFMARQC 500
 Db 483 TSAASIFFIERRPWRPAMKFRSGHPAYAEVPGV-EKEGFIVSEQ 530

RESULT 7

Q96E59 PRELIMINARY; PRT; 480 AA.
 AC Q96E59;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to RIKEN cDNA 1200007L24 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RA Strauberg R.;
RA EMBL; BC012885; AAH12885.1;
DR InterPro: IPR002165; Plexin_repeat.
DR Pfam: PF01437; PSI; 1.
SQ SEQUENCE 480 AA; 53912 MW; 53912 MW; F8DB0E2631BC7816 CRC64;

Query Match 41.9%; Score 1127.5; DB 4; Length 480;
Best Local Similarity 25.1%; Pred. No. 3e-50;
Matches 142; Conservative 72; Mismatches 158; Indels 33; Gaps 8;

QY 73 AMDTLPDNRTRVEDHNSYVRLYGPSEPHS-RELWVDVAEAFNSQVKIHTILSNTHRQ 131
DB 74 AVDT---NRASVGQDS-----PEPRSFDTLLDDGDNDNTQIE----- 108
QY 132 ASRVLSDFDPYGHPLRQIATIGFTFMGDVTHRMILTATQYVAPLMANFNPGYSDNST 191
DB 109 --RVNLSDFDPYGHFLREIIVATIGFTYTGTVHRLMTATQYIAPLMANFDPVSRNST 166
QY 192 VYFONGTVVQWHDVYVQWHDVYVQWHDVYVQWHDVYVQWHDVYVQWHDVYVQWHDV 251
DB 167 VRYFONGTALVQWHDVYVQWHDVYVQWHDVYVQWHDVYVQWHDVYVQWHDVYVQW 226
QY 252 VKTGLSDAFMILNPSDPVPESSRRSIFEVHRIELDPKSVTMSAVEFTPLPTCLQHRSCD 311
DB 227 VVGLSDAFVYVQWHDVYVQWHDVYVQWHDVYVQWHDVYVQWHDVYVQWHDVYVQW 286
QY 312 ACMSSDLTFCNCHWVLCRCSSGDFRYRQEWMDYGAEGRCMCEQFQDDEHDHDSASPDT 371
DB 287 PCVSSQIGFNCWCNKLQRCSSGDFRHRQDWDVSCPCPEKSKMCEPNETVETSTRTTT 346
QY 372 --SFSPYDGLTFTS---SSLFDSLTFTEDDTPKLPYAGGGLQ--NLSPTKTPGVHLG 425
DB 347 VGATTTFQVRLTTRAVTSQFTSLPTEDDTKIALHLKDNAGSDTSDAAEKKGGTLHAG 406
QY 426 TIVGIVLAVLLAAITLAGIYINGHTPSNAALFFTERPHHPWPAKFKRSHDPHSHYAEV 485
DB 407 LIIGILVILVATAILVTVMYHHPTSAASIFFIERPSRPWPAKFKRSGHSHYAEV 466
QY 486 PSGEKEGFEAEQC 500
DB 467 PVG-EKEGFIIVEQC 480

RESULT 8
Q9W2V9 PRELIMINARY; PRT; 625 AA.
AC Q9W2V9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG2221 protein (LD40707p).
GN CG2221.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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Db 505 TNTSTSSSGSTPVPTEPSVMSTRAPHATAYIKPGVDHSSDIHADGKVGNAELSKAEADNK 564

QY 423 HLGTVIGIVLAVLLAAIILAGIYINGHPTSNAALFFIERRPHHW 467

Db 565 NVGVAFGFMVPCICLVFAVTLWLFYARNPHTKSGQLLIQFRESOW 609

RESULT 9

Q18500 ID Q18500 PRELIMINARY; PRT; 476 AA.
AC Q18500;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE C3688.3 protein.
GN C3688.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilkinson J., Barlow K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z35597; CA84646.1; -;
SQ SEQUENCE 476 AA; 53918 MW; AC72884A06D57F4D CRC64;

Query Match 22.7%; Score 611; DB 5; Length 476;
Best Local Similarity 34.2%; Pred. No. 5.4e-46;
Matches 149; Conservative 65; Mismatches 160; Indels 62; Gaps 15;

QY 46 RRARESPGVSEPPORTOLS-----QDLGGTFLMDTLPDNRTRVDENHSHYVSRLLGPS 100

Db 62 RTARAAP-----IPKRLASEQDEEDIDPATATIP--PDVEVKNDMDIHQYQAEVGD 115

QY 101 EPHRELVDVVAEANRSOVKI-----HTILSNTHQASRVLSDFPFYGHPLRQITATG 156

Db 116 GETLKKYINVEQFMKPKAVGNTSHPLLSQSYRRVARGARLQFKFPYGHKMSMLTATG 175

QY 157 GFIFMGDVIHRLTATQVAPIMANFPGYSDNSTVYVFDNGTVFVVQWDHVLQGWEDK 216

Db 176 GFYIGDHSNWLAAATQYIAPLMANFHT-YLNNNSNIVVADDDGELFVVEWRNVQLKEDKDE 234

QY 217 GSFTFOAALHHDGRIVFAYKEIPMSVPEISSQHPVKTLGLSDAPMLN--PSPDVPESRR 274

Db 235 HSFTFQTLHKGDLVIFYDKDVPDVISNIDANHPVKLGISDAYMFKNHLHQAAVP--K 291

QY 275 RSIFEYHRIELDPKSVTSMASAVEFTPLPTCLQHRSCDACMSSDLT-FNCSCWCHVLRQ--- 330

Db 292 RVVIEYHRIEIAAQKIVSNTVILKQAQTCISDPTCDTCTNATLPHNCLWCHAKSHGG 351

QY 331 --CS--SGFDYRQEWMDYGAQAEGRMCE-DFQDEHDHAS--PDTSFSPYDGLTTTS 384

Db 352 PFCDEAGLHRRRHOHFWEGNQCYSKALYCDADDEDEYDEYDPSQLMPNGGH---TV 408

QY 385 SSLFIDSITTTDDTKLNPYAGGDCGLQNNLSFKTKGTGTPVHLGTIVGLVALLVAAILAG 444

Db 409 LPLADNMKTKDTKTTSEDSDEWKGHKKEPK-----GG 442

QY 445 IYINGHP--TSNAALF 458

Db 443 VATTAPVGTQAATF 458

RESULT 10

Q96SU9

ID Q96SU9 PRELIMINARY; PRT; 151 AA.
AC Q96SU9;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE CDNA FLJ14623 fis, clone NT2RP2000173.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK027529; BAB5178.1; -;
SQ SEQUENCE 151 AA; 16423 MW; F261A41CC9408347 CRC64;

Query Match 11.1%; Score 297.5; DB 4; Length 151;
Best Local Similarity 46.1%; Pred. No. 1.1e-18;
Matches 70; Conservative 24; Mismatches 51; Indels 7; Gaps 4;

QY 355 MCEDFODEDHDSDASPD--SFSPYDGLTTTS---SSLFIDSITTTEDDTKLNPPYAGGDL 409

Db 1 MCEPTEPVTSSRTTTTIGATTTFQFRLVTTTRAVTSQFPTSLPTEDDTKIALHLDKNGA 60

QY 410 Q-NLSPKTKGTPVHLGTIVGLVLAIVAAIILAGIYINGHPTSNAALFFIERRPHHP 468

Db 61 STDDSAEKKGGTLHAGLVILILVIALIVATLVVYVYHHPTSAASIFFIERRPSRWP 120

QY 469 AMKFRSHPDHSIYAEVPSGHEKEGFMEAEQC 500

Db 121 AMKFRSGHPAYAEVPGV-EKEGFIVSEQC 151

RESULT 11

ID Q04901 PRELIMINARY; PRT; 1161 AA.
AC Q04901;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE Entactin/nidogen.
OC Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE.
RX MEDLINE=93238676; PubMed=8477687;
RA Nakae H., Sugano M., Ishimori Y., Endo T., Obinata T.;
RT "Ascidian entactin/nidogen: Implication of evolution by shuffling two
RT kinds of cysteine-rich motifs.";
RL Eur. J. Biochem. 213:11-19(1993).
DR EMBL: D14038; BAA03127.1; -;
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000033; Ldl_receptor_rep.
DR InterPro: IPR003886; Nidogen_ext.
DR InterPro: IPR00716; Thyroglobulin_1.
DR InterPro: IPR000834; Zn_carboxypept.
DR Pfam: PF00058; ldl_recept_b; 4.
DR Pfam: PF00086; thyroglobulin_1; 3.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00135; LY; 4.
DR SMART: SM00539; NIDO; 1.
DR SMART: SM00211; TY; 3.


```
Db 461 CSECLTA-TDPCHGCHSLQRTFGDCVHSENLENWLDI-----SSGAKCKPKIQIIRSS 515
QY 362 EDHDSASPDTSFSP 375
Db 516 KEKTTVTWVGSFSP 529

RESULT 14
Q9UN95
ID Q9UN95 PRELIMINARY; PRT; 366 AA.
AC Q9UN95;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 20, Last annotation update)
DE Mucin 3 (Fragment).
GN MUC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON MUCOSA;
RX MEDLINE=99335363; PubMed=10405327;
RA Williams S.J., Munster D.J., Quin R.J., Gotley D.C., McCuckin M.A.;
RT "The MUC3 gene encodes a transmembrane mucin and is alternatively
spliced.";
RL Biochem. Biophys. Res. Commun. 261:83-89(1999).
DR EMBL; AF143371; AAD45882.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF01390; SEA; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50024; SEA; 1.
KW EGF-like domain; Glycoprotein.
FT NON_TER
FT SEQUENCE 366 AA; 40953 MW; 88F3F0E3F439A3C2 CRC64;

Query Match 4.1%; Score 111.5; DB 4; Length 366;
Best Local Similarity 25.0%; Pred. No. 0.18;
Matches 49; Conservative 28; Mismatches 98; Indels 21; Gaps 9;
```

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QY 182 FNPQYSDNSTVYFDNGTVFVQWDHVV--LQGWEDKGSFTFQAALHHDGRIVFAY---K 236
Db 77 FSPDLNDNTSQAYRDNKTFWQMKIFADMQGFTFKG---VEILSLRNGSIVVDYLVLL 133
QY 237 EIPMSVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRSIFEYHRIELDPKSVTMSAV 296
Db 134 EMPFS-POLESEYEQVKTTLKEG--LQNASQDVNSQDSQTLCF---KPDSTKVNNSKT 187
QY 297 EFTPLPTCLQHRSCDACMSDDLTF---NCSWCHVLQRCSSGFDRIYQEWMDYGCQAEAG 353
Db 188 ELTPAAIC---RRAAPTGYEEFYFPLVEATRLRCVTCTSGVDN-AIDCHQGCQVLETSG 243
QY 354 RMCEDFQDEHDSASP 369
Db 244 PTCRCYSTDTTHWFSGP 259
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```
RESULT 15
Q9H3Q6
ID Q9H3Q6 PRELIMINARY; PRT; 877 AA.
AC Q9H3Q6;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Intestinal mucin (fragment).
GN MUC3A.
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RX MEDLINE=21183349; PubMed=11289722;
RA Kyo K., Muto T., Nagawa H., Lathrop GM., Nakamura Y.;
RT "Associations of distinct variants of the intestinal mucin gene MUC3A
with ulcerative colitis and Crohn's disease.";
RL J. Hum. Genet. 46:5-20(2001).
DR EMBL; AB038784; BAB12118.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF01390; SEA; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50024; SEA; 1.
FT NON_TER
FT SEQUENCE 877 AA; 93720 MW; 09BE5E86BC838DFA CRC64;

Query Match 4.1%; Score 111.5; DB 4; Length 877;
Best Local Similarity 25.0%; Pred. No. 0.65;
Matches 49; Conservative 28; Mismatches 98; Indels 21; Gaps 9;
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Search completed: April 22, 2003, 16:07:49
Job time : 37 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:14:16 ; Search time 90 Seconds
(without alignments)
1144.706 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 500

Sequence: 1 MRGELWLLVLRARALS.....YAEVPSGHEKGFMEAEQC 500

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	500	100.0	500	4	Q9HCT9		Q9hct9 homo sapien
2	35	7.0	500	11	Q9CWV5		Q9cwv5 mus musculus
3	35	7.0	500	11	Q9LZV7		Q9lzv7 mus musculus
4	10	2.0	480	4	Q96E59		Q96e59 homo sapien
5	10	2.0	529	4	Q96PD9		Q96pd9 homo sapien
6	10	2.0	530	11	Q9DC11		Q9dc11 mus musculus
7	10	2.0	530	11	Q9LZV6		Q9lzv6 mus musculus
8	9	1.8	655	16	P94476		P94476 bacillus su
9	8	1.6	208	17	Q970I9		Q970i9 sulfolobus
10	8	1.6	224	16	Q9S2F8		Q9s2f8 streptomyce
11	8	1.6	317	2	Q54303		Q54303 streptomyce
12	8	1.6	363	17	Q9HQA6		Q9hqa6 halobacteri
13	8	1.6	429	16	Q9AC73		Q9ac73 staphylococ
14	8	1.6	472	16	Q9JYC8		Q9jyc8 neisseria m
15	8	1.6	472	16	Q9JTB1		Q9jtb1 neisseria m
16	8	1.6	476	5	Q18500		Q18500 caenorhabdi

054179 streptomyce	483	16	054179	17	1.6	8
Q911b4 streptomyce	510	16	Q9L1B4	18	1.6	8
Q3968 streptomyce	519	2	Q3968	19	1.6	8
Q8YKQ2 anabaena sp	562	16	Q8YKQ2	20	1.6	8
Q9W2V9 streptomyce	625	5	Q9W2V9	21	1.6	8
Q9Za45 streptomyce	751	2	Q9Za45	22	1.6	8
Q94958 homo sapien	924	4	Q94958	23	1.6	8
Q970el sulfolobus	1136	17	Q970El	24	1.6	8
P79120 bos taurus	68	6	P79120	25	1.4	7
Q9nm35 leishmania	79	5	Q9NM35	26	1.4	7
Q921e9 rickettsia	82	16	Q921E9	27	1.4	7
Q4852 lactobacilli	90	16	Q4852	28	1.4	7
Q54389 streptomyce	93	2	Q54389	29	1.4	7
Q9bpb6 inversidens	100	2	Q9Bpb6	30	1.4	7
Q9bpb4 inversidens	103	8	Q9Bpb4	31	1.4	7
Q9bpb3 lanceolaria	103	8	Q9Bpb3	32	1.4	7
Q9bpb1 anodonta wo	103	8	Q9Bpb1	33	1.4	7
Q52012 halobacteri	114	17	Q52012	34	1.4	7
Q985j4 rhizobium 1	116	16	Q985J4	35	1.4	7
P94859 klebsiella	122	2	P94859	36	1.4	7
Q8qkv6 ectocarpus	124	12	Q8QKV6	37	1.4	7
Q9le71 oryza sativ	133	10	Q9LE71	38	1.4	7
Q97g98 clostridium	133	16	Q97G98	39	1.4	7
Q8Z948 salmonella	147	16	Q8Z948	40	1.4	7
Q9a4t0 caulobacter	150	16	Q9A4T0	41	1.4	7
Q96su9 homo sapien	151	4	Q96SU9	42	1.4	7
Q9g0i9 quincuncina	151	8	Q9G0I9	43	1.4	7
Q9g0i8 fusconaia s	151	8	Q9G0I8	44	1.4	7
Q9g0i7 quincuncina	151	8	Q9G0I7	45	1.4	7
Q9g0i6 obovaria ro	151	8	Q9G0I6	46	1.4	7
Q9g0k4 quincuncina	151	8	Q9G0K4	47	1.4	7
Q9g0k3 quincuncina	151	8	Q9G0K3	48	1.4	7
Q9g0k2 quincuncina	151	8	Q9G0K2	49	1.4	7
Q9g0k0 obovaria un	151	8	Q9G0K0	50	1.4	7
Q9g0j9 obovaria ol	151	8	Q9G0J9	51	1.4	7
Q9g0j8 fusconaia e	151	8	Q9G0J8	52	1.4	7
Q9g0j5 fusconaia f	151	8	Q9G0J5	53	1.4	7
Q9g0j3 anodonta cy	151	8	Q9G0J3	54	1.4	7
Q9g0j2 cumberlandi	151	8	Q9G0J2	55	1.4	7
Q8yeul bruceella me	151	16	Q8YEUL	56	1.4	7
Q8tia6 methanosarc	164	17	Q8TLA6	57	1.4	7
Q97103 clostridium	166	16	Q97103	58	1.4	7
Q9a6m6 pseudomonas	170	2	Q9AQM6	59	1.4	7
Q9npa9 homo sapien	170	16	Q9NPA9	60	1.4	7
Q8zwm1 pyrobaculum	172	4	Q8ZWM1	61	1.4	7
Q94mq1 bacterioph	175	17	Q94MQ1	62	1.4	7
Q9a4j3 caulobacter	177	9	Q9A4J3	63	1.4	7
Q9y0w0 schistocerc	177	16	Q9Y0W0	64	1.4	7
Q9rt80 deinococcus	178	5	Q9RT80	65	1.4	7
Q9j3p3 avian infec	183	12	Q9J3P3	66	1.4	7
Q9j3p2 avian infec	183	12	Q9J3P2	67	1.4	7
Q9j3p1 avian infec	183	12	Q9J3P1	68	1.4	7
Q9j3p0 avian infec	183	12	Q9J3P0	69	1.4	7
Q9j3n9 avian infec	183	12	Q9J3N9	70	1.4	7
Q9j3n8 avian infec	183	12	Q9J3N8	71	1.4	7
Q8uij1 agrobacteri	186	16	Q8UIJ1	72	1.4	7
Q95sv0 drosophila	186	16	Q95SV0	73	1.4	7
Q9me60 alasmidonta	189	5	Q9ME60	74	1.4	7
Q9mqv0 strophitus	194	8	Q9MQV0	75	1.4	7
Q9mqu5 lasmignona c	194	8	Q9MQU5	76	1.4	7
Q9mqu4 lasmignona c	195	8	Q9MQU4	77	1.4	7
Q9csc7 mus musculu	195	11	Q9CSC7	78	1.4	7
Q8rtq0 uncultured	196	2	Q8RQT0	79	1.4	7
Q8wcr7 lampisilis p	196	2	Q8WCR7	80	1.4	7
Q8wcr4 lampisilis a	197	8	Q8WCR4	81	1.4	7
Q8wcr3 lampisilis a	197	8	Q8WCR3	82	1.4	7
Q8wcr2 lampisilis s	197	8	Q8WCR2	83	1.4	7
Q8wcr1 lampisilis s	197	8	Q8WCR1	84	1.4	7
Q8wcr0 lampisilis s	197	8	Q8WCR0	85	1.4	7
Q8wcq9 lampisilis a	197	8	Q8WCQ9	86	1.4	7
Q8wcq7 lampisilis a	197	8	Q8WCQ7	87	1.4	7
Q8wcq6 lampisilis a	197	8	Q8WCQ6	88	1.4	7
Q8wcq5 lampisilis a	197	8	Q8WCQ5	89	1.4	7

90	7	1.4	197	8	Q8WC6	Q8wcq6 lampsillis a	163	7	1.4	223	12	Q91NK5	Q91nk5 avian infec
91	7	1.4	197	8	Q8WCQ2	Q8wcq2 lampsillis o	164	7	1.4	223	12	Q91LNK4	Q91lnk4 avian infec
92	7	1.4	197	8	Q8WCQ0	Q8wcq0 obliquaria	165	7	1.4	223	12	Q91OE2	Q91oe2 avian infec
93	7	1.4	197	8	Q8WJ1	Q8wj1 lampsillis a	166	7	1.4	223	14	P97967	P97967 unidentified
94	7	1.4	197	8	Q8WJ0	Q8wj0 lampsillis p	167	7	1.4	224	12	Q986K0	Q986k0 rhizobium l
95	7	1.4	199	8	Q9S512	Q9s512 lampsillis o	168	7	1.4	225	16	Q9J4A6	Q9j4a6 avian infec
96	7	1.4	199	8	Q9S513	Q9s513 obliquaria	169	7	1.4	225	12	Q9J4B3	Q9j4b3 avian infec
97	7	1.4	202	5	Q9N9A7	Q9n9a7 leishmania	170	7	1.4	225	12	Q99AS5	Q99as5 avian infec
98	7	1.4	204	2	Q8RQ57	Q8rq57 uncultured	171	7	1.4	225	12	Q91SA1	Q91sa1 avian infec
99	7	1.4	204	8	Q33836	Q33836 amblema pli	172	7	1.4	225	12	Q91SA0	Q91sa0 avian infec
100	7	1.4	204	8	Q33685	Q33685 anodonta cy	173	7	1.4	225	12	Q91S99	Q91s99 avian infec
101	7	1.4	204	8	Q35084	Q35084 mutela rost	174	7	1.4	225	12	Q91S98	Q91s98 avian infec
102	7	1.4	205	17	Q8ZUF7	Q8zuf7 pyrobaculum	175	7	1.4	225	12	Q91GB7	Q91gb7 avian infec
103	7	1.4	206	12	Q82614	Q82614 avian infec	176	7	1.4	225	12	Q91OH8	Q91oh8 avian infec
104	7	1.4	208	8	Q8SFU0	Q8sfu0 pseudanodon	177	7	1.4	225	12	Q91JX1	Q91jx1 avian infec
105	7	1.4	209	2	P94796	P94796 francisella	178	7	1.4	230	16	Q8UJH6	Q8ujh6 agrobacteri
106	7	1.4	209	8	Q8SK63	Q8sk63 unio tumidi	179	7	1.4	234	4	Q9H5C5	Q9h5c5 homo sapien
107	7	1.4	210	8	Q94R01	Q94r01 giebula rot	180	7	1.4	235	8	Q956B4	Q956b4 anodonta wo
108	7	1.4	210	8	Q94R00	Q94r00 actinonaias	181	7	1.4	242	6	Q9BFG2	Q9bfg2 talpa alta
109	7	1.4	210	8	Q94QZ8	Q94qz8 unio tumidi	182	7	1.4	243	5	Q95T03	Q95t03 drosophila
110	7	1.4	210	8	Q94QZ7	Q94qz7 fusconala f	183	7	1.4	247	5	O16379	O16379 caenorhabdi
111	7	1.4	210	8	Q94QZ6	Q94qz6 pyganodon g	184	7	1.4	260	16	Q92W83	Q92w83 rhizobium m
112	7	1.4	210	8	Q94QZ5	Q94qz5 coelatura a	185	7	1.4	260	16	Q92W83	Q92w83 rhizobium m
113	7	1.4	210	8	Q94QZ3	Q94qz3 mutela dubi	186	7	1.4	271	16	Q9X130	Q9x130 thermotoga
114	7	1.4	210	8	Q94QZ0	Q94qz0 strophitus	187	7	1.4	278	2	Q9A152	Q9a152 burkholderi
115	7	1.4	210	8	Q94QY5	Q94qy5 monocondyla	188	7	1.4	282	3	Q12057	Q12057 saccharomyc
116	7	1.4	210	8	Q94QY1	Q94qy1 cyrtonalas	189	7	1.4	293	2	O50269	O50269 agrobacteri
117	7	1.4	210	8	Q94QX9	Q94qx9 elliptio di	190	7	1.4	294	17	Q8TQJ7	Q8tqj7 methanosarc
118	7	1.4	210	8	Q94QX7	Q94qx7 cumberlandi	191	7	1.4	294	16	Q93OC6	Q93oc6 rhizobium m
119	7	1.4	210	8	Q94QX6	Q94qx6 pleurobema	192	7	1.4	301	6	Q9BFE6	Q9bfe6 tarsius ban
120	7	1.4	210	8	Q94QX5	Q94qx5 gonidea ang	193	7	1.4	304	10	Q91PL2	Q91pl2 arabidopsis
121	7	1.4	210	8	Q94QX4	Q94qx4 toxolasma l	194	7	1.4	310	4	O75938	O75938 homo sapien
122	7	1.4	210	8	Q94QX3	Q94qx3 quadrula qu	195	7	1.4	312	16	Q92BGO	Q92bg0 streptomyce
123	7	1.4	213	4	Q9Y4U6	Q9y4u6 homo sapien	196	7	1.4	318	2	Q93F49	Q93f49 pseudomonas
124	7	1.4	213	4	Q9UQN3	Q9uqn3 homo sapien	197	7	1.4	318	16	Q8YCJ2	Q8ycj2 bruceella me
125	7	1.4	214	16	Q92R50	Q92r50 rhizobium m	198	7	1.4	318	16	Q8YCJ2	Q8ycj2 bruceella me
126	7	1.4	215	8	Q9XW4	Q9xmw4 fusconala f	199	7	1.4	321	16	Q916G4	Q916g4 pseudomonas
127	7	1.4	215	8	Q9XW8	Q9xmw8 actinonaias	200	7	1.4	321	16	Q916G4	Q916g4 pseudomonas
128	7	1.4	215	8	Q8WB66	Q8wb66 anodonta cy	201	7	1.4	322	16	Q9RK51	Q9rk51 streptomyce
129	7	1.4	215	14	P97975	P97975 unidentified	202	7	1.4	323	16	Q8XPX0	Q8xpx0 raistonia s
130	7	1.4	216	8	Q9XK72	Q9xk72 cumberlandi	203	7	1.4	327	16	Q49822	Q49822 mycobacteri
131	7	1.4	216	8	Q9XK71	Q9xk71 elliptio di	204	7	1.4	328	6	Q9BFC4	Q9bfc4 manis penta
132	7	1.4	216	8	Q9XK23	Q9xk23 pleurobema	205	7	1.4	329	6	Q9BFE1	Q9bfe1 artibeus ja
133	7	1.4	216	8	Q9XW48	Q9xmw8 alasmidonta	206	7	1.4	329	6	Q9BFD8	Q9bfd8 nycteris th
134	7	1.4	216	8	Q9XW7	Q9xmw7 lasmigona c	207	7	1.4	329	11	Q99NT8	Q99nt8 dipodomys h
135	7	1.4	216	8	Q9XW6	Q9xmw6 pyganodon g	208	7	1.4	330	5	Q9BMW8	Q9bmw8 trypanosoma
136	7	1.4	216	8	Q9XW5	Q9xmw5 strophitus	209	7	1.4	330	6	Q9BFG8	Q9bfg8 choleopus h
137	7	1.4	216	8	Q9XW3	Q9xmw3 quadrula qu	210	7	1.4	330	6	Q9BFG8	Q9bfg8 choleopus h
138	7	1.4	216	8	Q9TFB1	Q9tfb1 amblema pli	211	7	1.4	330	6	Q9BFG7	Q9bfg7 choleopus d
139	7	1.4	216	8	Q9XW0	Q9xmw0 ligumia nas	212	7	1.4	330	6	Q9BFG6	Q9bfg6 euphractus
140	7	1.4	216	8	Q9XWV7	Q9xmw7 lampsillis c	213	7	1.4	330	6	Q9BFG5	Q9bfg5 euphractus
141	7	1.4	216	8	Q9XWV6	Q9xmw6 lampsillis c	214	7	1.4	330	6	Q9BFG4	Q9bfg4 taenidia te
142	7	1.4	216	8	Q9XWV5	Q9xmw5 lampsillis f	215	7	1.4	330	6	Q9BFG3	Q9bfg3 myrmecophag
143	7	1.4	216	8	Q9XW4	Q9xmw4 villosa van	216	7	1.4	330	6	Q9BFG0	Q9bfg0 sorex arane
144	7	1.4	216	8	Q9TFB0	Q9tfb0 villosa van	217	7	1.4	330	6	Q9BFF8	Q9bff8 trichechus
145	7	1.4	217	5	Q23973	Q23973 drosophila	218	7	1.4	330	6	Q9BFF7	Q9bff7 procavia ca
146	7	1.4	217	5	Q9V5J7	Q9vsj7 drosophila	219	7	1.4	330	6	Q9BFE6	Q9bfe6 loxodonta a
147	7	1.4	219	6	Q9BFF9	Q9bff9 echinops te	220	7	1.4	330	6	Q9BFE5	Q9bfe5 macroscelid
148	7	1.4	219	16	Q98P47	Q98p47 rhizobium l	221	7	1.4	330	6	Q9BFF4	Q9bff4 elephantulu
149	7	1.4	220	2	Q9RQZ1	Q9rqz1 staphylococ	222	7	1.4	330	6	Q9BFF1	Q9bff1 sylvilaqus
150	7	1.4	220	6	Q9BFF2	Q9bff2 tagelaphus	223	7	1.4	330	6	Q9BFF0	Q9bff0 ochotona hy
151	7	1.4	220	16	Q99QX4	Q99qx4 staphylococ	224	7	1.4	330	6	Q9BFE8	Q9bfe8 tupia mino
152	7	1.4	221	6	Q9BFF3	Q9bff3 orycteropus	225	7	1.4	330	6	Q9BFE7	Q9bfe7 lemur catta
153	7	1.4	221	6	Q9BFE9	Q9bfe9 cynocephalu	226	7	1.4	330	6	Q9BFE0	Q9bfe0 pteropus gl
154	7	1.4	221	11	Q99NT7	Q99nt7 heteroceph	227	7	1.4	330	6	Q9BFD9	Q9bfd9 rousettus l
155	7	1.4	221	6	Q9BFG9	Q9bfg9 cavia tschu	228	7	1.4	330	6	Q9BFD7	Q9bfd7 megaptera n
156	7	1.4	222	8	Q8WEU0	Q8weu0 didelphis m	229	7	1.4	330	6	Q9BFD5	Q9bfd5 tursiops tr
157	7	1.4	223	12	Q91SA4	Q91sa4 lampsillis c	230	7	1.4	330	6	Q9BFD5	Q9bfd5 tursiops tr
158	7	1.4	223	12	Q91SA3	Q91sa3 avian infec	231	7	1.4	330	6	Q9BFD4	Q9bfd4 lama glama
159	7	1.4	223	12	Q91SA4	Q91sa4 avian infec	232	7	1.4	330	6	Q9BFD3	Q9bfd3 sus scrofa
160	7	1.4	223	12	Q91S96	Q91s96 avian infec	233	7	1.4	330	6	Q9BFD2	Q9bfd2 okapia john
161	7	1.4	223	12	Q91S95	Q91s95 avian infec	234	7	1.4	330	6	Q9BFD1	Q9bfd1 equus cabal
162	7	1.4	223	12	Q91NK6	Q91nk6 avian infec	235	7	1.4	330	6	Q9BFD0	Q9bfd0 ceratotheri

236	7	1.4	330	6	Q9BFC9	Q9bfc9 tapirus ind	309	7	1.4	463	4	Q9H9V9	Q9h9v9 homo sapien
237	7	1.4	330	6	Q9BFC8	Q9bfc8 felis silve	310	7	1.4	463	5	Q93WX6	Q93wx6 arabidopsis
238	7	1.4	330	6	Q9BFC7	Q9bfc7 leopards p	311	7	1.4	469	5	O44321	O44321 tenebrio mo
239	7	1.4	330	6	Q9BFC6	Q9bfc6 panthera on	312	7	1.4	469	5	Q20752	Q20752 caenorhabdi
240	7	1.4	330	6	Q9BFC5	Q9bfc5 canis fami	313	7	1.4	469	16	Q915N9	Q915n9 pseudomonas
241	7	1.4	330	11	Q99NU6	Q99nu6 castor cana	314	7	1.4	470	2	Q60154	Q60154 pelobacter
242	7	1.4	330	11	Q99NU5	Q99nu5 muscardinus	315	7	1.4	471	11	Q35162	Q35162 rattus norv
243	7	1.4	330	11	Q99NU4	Q99nu4 pedetes cap	316	7	1.4	488	5	Q18760	Q18760 caenorhabdi
244	7	1.4	330	11	Q99NU0	Q99nu0 hystrix bra	317	7	1.4	497	16	Q98B98	Q98b98 rhizobium l
245	7	1.4	330	11	Q99NT9	Q99nt9 erethizon d	318	7	1.4	498	16	Q82L78	Q82l78 salmonella
246	7	1.4	330	11	Q99NT5	Q99nt5 hydrochoeru	319	7	1.4	498	16	Q822C9	Q822c9 salmonella
247	7	1.4	330	11	Q99NT4	Q99nt4 myocastor c	320	7	1.4	506	16	Q9K0Q3	Q9k0q3 neisseria m
248	7	1.4	330	11	Q99NT3	Q99nt3 agouti tacz	321	7	1.4	506	16	Q9JVT2	Q9jvt2 neisseria m
249	7	1.4	331	6	Q9BFC1	Q9bfc1 condylura c	322	7	1.4	512	8	Q956C8	Q956c8 inversidens
250	7	1.4	331	11	Q99NU7	Q99nu7 tamias stri	323	7	1.4	519	10	Q9FJ09	Q9fj09 arabidopsis
251	7	1.4	331	11	Q99NU3	Q99nu3 mus musculu	324	7	1.4	520	10	Q9SLD2	Q9slld2 arabidopsis
252	7	1.4	331	11	Q99NU2	Q99nu2 rattus norv	325	7	1.4	525	16	Q9K634	Q9k634 bacillus ha
253	7	1.4	331	11	Q99NU1	Q99nu1 cricetus	326	7	1.4	525	16	Q9X0Y8	Q9xuy8 ralstonia s
254	7	1.4	333	16	Q97ER9	Q97er9 clostridium	327	7	1.4	526	10	Q9SJE3	Q9sje3 arabidopsis
255	7	1.4	336	16	Q8YUV2	Q8yuv2 anabaena sp	328	7	1.4	528	5	Q9VTO8	Q9vtn8 drosophila
256	7	1.4	338	16	Q8YU17	Q8yu17 brucella me	329	7	1.4	533	2	Q93NX3	Q93nx3 streptomyce
257	7	1.4	340	5	Q9VNL5	Q9vnl5 drosophila	330	7	1.4	535	9	Q9MBL8	Q9mb18 corynebacte
258	7	1.4	346	16	Q8ZDS8	Q8zds8 yersinia pe	331	7	1.4	541	16	Q91493	Q91493 pseudomonas
259	7	1.4	346	16	Q8YCU5	Q8ycu5 brucella me	332	7	1.4	542	12	Q92377	Q92377 bombyx mori
260	7	1.4	347	16	Q92XA5	Q92xa5 rhizobium m	333	7	1.4	557	10	Q8RWK1	Q8rwl1 arabidopsis
261	7	1.4	352	16	Q97KT1	Q97kt1 clostridium	334	7	1.4	569	10	Q9FP06	Q9fp06 oryza sativ
262	7	1.4	358	9	Q9FZT1	Q9fzt1 pseudomonas	335	7	1.4	574	2	Q9AQH1	Q9aqh1 pseudomonas
263	7	1.4	365	15	Q97R0	Q97r0 human immun	336	7	1.4	574	16	Q9HWG7	Q9hwg7 pseudomonas
264	7	1.4	365	16	Q92TG9	Q92tg9 rhizobium m	337	7	1.4	592	16	Q67937	Q67937 aquifex aeo
265	7	1.4	370	11	Q9DCX3	Q9dcx3 mus musculu	338	7	1.4	599	6	O19112	O19112 sus scrofa
266	7	1.4	372	2	Q54025	Q54025 salmonella	339	7	1.4	609	5	Q22680	Q22680 caenorhabdi
267	7	1.4	372	2	Q54026	Q54026 salmonella	340	7	1.4	614	5	Q9W3P8	Q9w3p8 drosophila
268	7	1.4	372	2	Q54027	Q54027 salmonella	341	7	1.4	623	17	Q971X1	Q971x1 sulfolobus
269	7	1.4	372	2	Q54028	Q54028 salmonella	342	7	1.4	626	16	Q9KYP5	Q9kyp5 streptomyce
270	7	1.4	372	2	Q54029	Q54029 salmonella	343	7	1.4	627	16	Q98PG2	Q98pg2 mycoplasma
271	7	1.4	372	2	Q54030	Q54030 salmonella	344	7	1.4	630	1	Q93675	Q93675 sulfolobus
272	7	1.4	372	2	Q54031	Q54031 salmonella	345	7	1.4	643	16	Q9KMQ2	Q9kmq2 vibrio chol
273	7	1.4	372	2	Q54032	Q54032 salmonella	346	7	1.4	648	17	Q8TH20	Q8th20 methanosarc
274	7	1.4	372	2	Q54033	Q54033 salmonella	347	7	1.4	653	16	Q9RDB5	Q9rdb5 streptomyce
275	7	1.4	372	2	Q54034	Q54034 salmonella	348	7	1.4	662	4	Q9UFR7	Q9ufr7 homo sapien
276	7	1.4	372	2	Q54035	Q54035 salmonella	349	7	1.4	680	10	Q8W0I8	Q8w0i8 oryza sativ
277	7	1.4	372	2	Q54036	Q54036 salmonella	350	7	1.4	693	3	Q00141	Q00141 aspergillus
278	7	1.4	372	2	Q54037	Q54037 salmonella	351	7	1.4	723	16	Q8YD09	Q8ydy9 brucella me
279	7	1.4	372	2	Q54038	Q54038 salmonella	352	7	1.4	731	10	Q9AKD1	Q9akd1 arabidopsis
280	7	1.4	372	2	Q54039	Q54039 salmonella	353	7	1.4	745	13	Q9PVS3	Q9pvs3 cyprinus ca
281	7	1.4	372	2	Q54040	Q54040 salmonella	354	7	1.4	751	10	O48802	O48802 arabidopsis
282	7	1.4	372	16	Q8Z490	Q8z490 salmonella	355	7	1.4	754	5	Q8SXJ1	Q8sxj1 drosophila
283	7	1.4	374	16	Q92U19	Q92uy9 rhizobium m	356	7	1.4	763	10	Q9FZ11	Q9fz11 arabidopsis
284	7	1.4	376	11	Q92Z24	Q92z24 rattus norv	357	7	1.4	769	16	Q97IS9	Q97is9 clostridium
285	7	1.4	379	16	Q92SB1	Q92sb1 rhizobium m	358	7	1.4	773	16	Q97J97	Q97j97 clostridium
286	7	1.4	382	2	Q9RHC3	Q9rhc3 bradyrhizob	359	7	1.4	782	10	P92988	P92988 arabidopsis
287	7	1.4	394	17	Q58179	Q58179 pyrococcus	360	7	1.4	803	4	Q96Q00	Q96q00 homo sapien
288	7	1.4	400	2	Q52293	Q52293 pseudomonas	361	7	1.4	839	17	Q8TQ74	Q8tq74 methanosarc
289	7	1.4	401	4	Q9H970	Q9h970 homo sapien	362	7	1.4	862	16	Q8RES2	Q8res2 fusobacteri
290	7	1.4	402	17	Q97Z99	Q97z99 sulfolobus	363	7	1.4	885	16	Q87658	Q87658 salmonella
291	7	1.4	404	16	Q9JWX3	Q9jwx3 neisseria m	364	7	1.4	891	16	Q92JJC2	Q92jc2 rickettsia
292	7	1.4	416	5	Q96360	Q96360 hyphantria	365	7	1.4	903	12	Q8VBL6	Q8vbl6 powassan vi
293	7	1.4	417	4	Q96EU8	Q96eu8 homo sapien	366	7	1.4	920	5	Q960B9	Q960b9 drosophila
294	7	1.4	417	11	Q92LW7	Q92lw7 cricetus	367	7	1.4	920	5	Q9VBP7	Q9vpb7 drosophila
295	7	1.4	420	16	Q8YU59	Q8yu59 anabaena sp	368	7	1.4	927	16	Q981V0	Q981v0 rhizobium l
296	7	1.4	421	16	Q9EX44	Q9ex44 streptomyce	369	7	1.4	936	5	Q9N910	Q9n910 trypanosoma
297	7	1.4	422	11	Q88228	Q88228 rattus norv	370	7	1.4	950	13	Q9YHC9	Q9ync9 xenopus lae
298	7	1.4	425	16	Q9KZ22	Q9kz22 streptomyce	371	7	1.4	953	16	P73173	P73173 synchocyst
299	7	1.4	430	16	Q97HA1	Q97ha1 clostridium	372	7	1.4	966	5	Q9U3P1	Q9u3p1 caenorhabdi
300	7	1.4	433	2	Q9ZA36	Q9za36 streptomyce	373	7	1.4	967	13	Q57579	Q57579 gallus gall
301	7	1.4	451	16	Q9HYK0	Q9hyk0 pseudomonas	374	7	1.4	999	16	Q9Z517	Q9z517 streptomyce
302	7	1.4	452	3	Q9Y7L5	Q9y7l5 schizosacch	375	7	1.4	1014	6	O62805	O62805 turlops tr
303	7	1.4	452	5	Q9N196	Q9n196 physarum po	376	7	1.4	1071	16	O69695	O69695 mycobacteri
304	7	1.4	452	11	Q9CXM9	Q9cxm9 mus musculu	377	7	1.4	1092	2	Q54099	Q54099 streptococc
305	7	1.4	454	5	Q9W4S1	Q9w4s1 drosophila	378	7	1.4	1096	16	Q9ABV4	Q9abv4 caulobacter
306	7	1.4	454	5	Q8SZ66	Q8sz66 drosophila	379	7	1.4	1184	4	O75339	O75339 homo sapien
307	7	1.4	456	5	Q17675	Q17675 caenorhabdi	380	7	1.4	1241	4	Q14148	Q14148 homo sapien
308	7	1.4	458	2	Q9FDT7	Q9fdt7 pseudomonas	381	7	1.4	1245	12	O9YTO9	O9ytc9 atelline her

382	7	1.4	1262	4	075163	075163 homo sapien	455	6	1.2	73	12	091FP8	091fp8 chilo iride
383	7	1.4	1270	10	09L129	09l129 oryza sativ	456	6	1.2	74	2	093CH9	093ch9 bacillus su
384	7	1.4	1298	10	09LSA4	09lsa4 arabidopsis	457	6	1.2	74	6	09N068	09n068 macaca fasc
385	7	1.4	1308	17	09V2G5	09v2g5 pyrococcus	458	6	1.2	74	10	09SDN7	09sdn7 nicotiana t
386	7	1.4	1323	4	096RG2	096rg2 homo sapien	459	6	1.2	74	16	08Y200	08y200 anabaena sp
387	7	1.4	1421	2	09L8C9	09l8c9 polyangium	460	6	1.2	77	16	08RDS1	08rdsl fusobacteri
388	7	1.4	1421	2	09KJ00	09kj00 streptomyce	461	6	1.2	77	5	003622	003622 plasmodium
389	7	1.4	1505	2	09F0D7	09f0d7 streptomyce	462	6	1.2	78	12	08V717	08v717 simian herp
390	7	1.4	1628	10	09LNE9	09lne9 arabidopsis	463	6	1.2	78	12	089339	089339 paramecium
391	7	1.4	1698	5	09V5J8	09v5j8 drosophila	464	6	1.2	79	5	0872C7	0872c7 dictyosteli
392	7	1.4	1759	5	09XTP8	09xtp8 plasmodium	465	6	1.2	79	5	095MH4	095mh4 pan troglod
393	7	1.4	1839	2	030765	030765 streptomyce	466	6	1.2	80	6	095MH3	095mh3 gorilla gor
394	7	1.4	1858	12	091PR6	091pr6 squash mosa	467	6	1.2	80	6	095MH2	095mh2 pongo pygna
395	7	1.4	2118	17	08T161	08t161 methanosarc	468	6	1.2	80	6	095MH1	095mh1 papio anubi
396	7	1.4	2126	16	094996	094996 mycobacteri	469	6	1.2	80	6	095MH0	095mh0 macaca mula
397	7	1.4	2391	5	027732	027732 plasmodium	470	6	1.2	80	6	095WG9	095wg9 macaca sile
398	7	1.4	3670	16	0924X5	0924x5 streptomyce	471	6	1.2	80	6	0913U4	0913u4 foot-and-mo
399	7	1.4	3944	5	018667	018667 caenorhabdi	472	6	1.2	80	12	09KN43	09kn43 vibrio chol
400	7	1.4	4268	16	08XFX2	08xfx2 raistonia s	473	6	1.2	81	5	09VPK9	09vpk9 drosophila
401	6	1.2	15	2	09R4Y0	09r4y0 pseudomonas	474	6	1.2	81	10	09LSW4	09lsw4 arabidopsis
402	6	1.2	20	10	09SBE8	09sbe8 zea mays (m	475	6	1.2	82	2	08RP85	08rp85 streptococc
403	6	1.2	26	2	005605	005605 pseudomonas	476	6	1.2	82	12	09Q3H8	09q3h8 hepatitis c
404	6	1.2	27	11	035837	035837 rattus sp.	477	6	1.2	82	12	09Q3H7	09q3h7 hepatitis c
405	6	1.2	28	15	073626	073626 human immun	478	6	1.2	82	12	09Q3H6	09q3h6 hepatitis c
406	6	1.2	35	11	09JW75	09jmw75 mus musculu	479	6	1.2	82	15	074089	074089 human immun
407	6	1.2	38	11	09ES99	09es99 rattus norv	480	6	1.2	83	2	09AQ40	09aq40 vibrio chol
408	6	1.2	43	4	014334	014334 homo sapien	481	6	1.2	83	12	09WGP5	09wgp5 human papil
409	6	1.2	43	4	014362	014362 homo sapien	482	6	1.2	83	12	09WGD9	09wgd9 human papil
410	6	1.2	43	11	064720	064720 rattus norv	483	6	1.2	83	12	09W884	09w884 human papil
411	6	1.2	45	12	068590	068590 hepatitis c	484	6	1.2	83	16	09ADE4	09ade4 streptomyce
412	6	1.2	45	12	068591	068591 hepatitis c	485	6	1.2	85	5	09VDM5	09vdm5 drosophila
413	6	1.2	45	12	068592	068592 hepatitis c	486	6	1.2	85	10	09C755	09c755 arabidopsis
414	6	1.2	45	12	068602	068602 hepatitis c	487	6	1.2	87	15	09YBY5	09yby5 human immun
415	6	1.2	45	12	068603	068603 hepatitis c	488	6	1.2	87	15	09YVC0	09yvc0 human immun
416	6	1.2	47	2	047111	047111 escherichia	489	6	1.2	88	2	087566	087566 bacillus ps
417	6	1.2	48	16	099WX4	099wx4 staphylococ	490	6	1.2	88	16	08Y522	08y522 listeria mo
418	6	1.2	52	13	09PWG0	09pwg0 coturnix co	491	6	1.2	88	17	09HNW9	09hnw9 halobacteri
419	6	1.2	55	16	09KVV7	09kvv7 vibrio chol	492	6	1.2	89	2	093L81	093l81 bacillus sp
420	6	1.2	56	17	08TXH4	08txh4 methanopyru	493	6	1.2	89	2	093L80	093l80 bacillus sp
421	6	1.2	58	15	P82290	P82290 anopheles g	494	6	1.2	89	2	093L77	093l77 bacillus sp
422	6	1.2	58	11	09Q238	09q238 mus musculu	495	6	1.2	89	16	09PQ79	09pq79 ureaplasma
423	6	1.2	59	2	09L7E0	09l7e0 synchococc	496	6	1.2	90	16	09PF53	09pf53 xylella fas
424	6	1.2	60	1	08X244	08x244 haloarcula	497	6	1.2	90	5	09VWN6	09vwn6 drosophila
425	6	1.2	61	2	09L7D8	09l7d8 synchococc	498	6	1.2	91	5	09VW03	09vw03 drosophila
426	6	1.2	60	5	095085	095085 caenorhabdi	499	6	1.2	91	17	027563	027563 methanobact
427	6	1.2	62	16	0935E1	0935el salmonella	500	6	1.2	92	11	091265	091265 sigmodon hi
428	6	1.2	63	4	09BXY1	09bxy1 homo sapien	501	6	1.2	92	12	091FL2	091fl2 chilo iride
429	6	1.2	66	2	085696	085696 streptomyce	502	6	1.2	92	6	09GLK8	09glk8 oryctolagus
430	6	1.2	66	16	09EWS5	09ews5 streptomyce	503	6	1.2	93	10	09C6F1	09c6f1 arabidopsis
431	6	1.2	67	2	053997	053997 nodularia s	504	6	1.2	93	16	09RJ49	09rj49 streptomyce
432	6	1.2	67	2	053999	053999 nodularia s	505	6	1.2	93	17	0972V4	0972v4 sulfolobus
433	6	1.2	67	2	054001	054001 nodularia s	506	6	1.2	94	5	09VTK4	09vtk4 drosophila
434	6	1.2	67	2	093E85	093e85 nodularia h	507	6	1.2	94	8	094YM4	094ym4 rana nigrom
435	6	1.2	67	2	093E83	093e83 nodularia s	508	6	1.2	94	10	08S3J7	08s3j7 oryza sativ
436	6	1.2	67	2	093E82	093e82 nodularia s	509	6	1.2	94	16	098H94	098h94 rhizobium l
437	6	1.2	67	2	093E80	093e80 nodularia b	510	6	1.2	94	16	08YHS5	08yhs5 bruceella me
438	6	1.2	67	2	093E78	093e78 nodularia s	511	6	1.2	94	17	082ZB9	082zb9 pyrobaculum
439	6	1.2	67	2	093E76	093e76 nodularia s	512	6	1.2	95	2	09S501	09s501 nodularia s
440	6	1.2	67	2	093E74	093e74 nodularia s	513	6	1.2	95	2	09S429	09s429 nodularia s
441	6	1.2	67	2	093E72	093e72 nodularia s	514	6	1.2	95	2	09S427	09s427 nodularia s
442	6	1.2	67	2	093206	0932u6 nodularia s	515	6	1.2	95	2	09S425	09s425 nodularia s
443	6	1.2	67	2	093205	0932u5 nodularia s	516	6	1.2	95	2	09S424	09s424 nodularia s
444	6	1.2	68	5	09N626	09n626 mytilus edu	517	6	1.2	95	2	093NN4	093nn4 nodularia s
445	6	1.2	68	5	09NAU6	09nau6 mytilus edu	518	6	1.2	95	2	093NN2	093nn2 nodularia h
446	6	1.2	69	12	08QWH6	08qwh6 human coxa	519	6	1.2	95	2	09R310	09r310 nodularia s
447	6	1.2	70	2	08VWF0	08vmf0 pseudomonas	520	6	1.2	95	10	08RU85	08ru85 arabidopsis
448	6	1.2	70	4	09BS22	09bs22 homo sapien	521	6	1.2	95	16	09L1Y7	09l1y7 streptomyce
449	6	1.2	70	12	09WIW0	09wiw0 human papil	522	6	1.2	96	6	095KX1	095kx1 canis famli
450	6	1.2	71	16	034408	034408 bacillus su	523	6	1.2	96	16	092BM4	092bm4 listeria in
451	6	1.2	72	5	09NAT8	09nat8 mytilus edu	524	6	1.2	96	16	08Y734	08y734 listeria mo
452	6	1.2	72	12	09J8B1	09j8b1 spidoptera	525	6	1.2	98	2	09RAG1	09rag1 planktothri
453	6	1.2	72	17	0979M7	0979m7 thermoplasm	526	6	1.2	98	16	09RWN2	09rwn2 deinococcus
454	6	1.2	73	12	090728	090728 human papil	527	6	1.2	99	16	092GM5	092gm5 rickettsia

528	6	1.2	99	16	P74283	P74283 synechocyst	601	1.2	128	5	O76888	O76888 drosophila
529	6	1.2	100	4	Q9H377	Q9H377 homo sapien	602	1.2	128	6	O8SQ46	O8SQ46 macaca fasc
530	6	1.2	100	16	Q9A774	Q9A774 caulobacter	603	1.2	128	6	O8SP13	O8SP13 macaca fasc
531	6	1.2	101	2	Q9F3Y8	Q9F3Y8 oscillatori	604	1.2	129	4	Q9H2Q1	Q9H2Q1 homo sapien
532	6	1.2	101	2	Q9F2E8	Q9F2E8 spirulina s	605	1.2	129	16	Q98K04	Q98K04 rhizobium 1
533	6	1.2	101	2	Q9F4A5	Q9F4A5 cyanobacter	606	1.2	130	2	Q9F7V9	Q9F7V9 mycobacteri
534	6	1.2	101	6	O62721	O62721 papio hamad	607	1.2	130	2	Q9KH54	Q9KH54 mycobacteri
535	6	1.2	102	5	Q9VUX2	Q9VUX2 drosophila	608	1.2	130	5	Q9TY27	Q9TY27 caenorhabdi
536	6	1.2	102	10	Q9CA51	Q9CA51 arabidopsis	609	1.2	130	10	Q9FK00	Q9FK00 arabidopsis
537	6	1.2	102	17	O28468	O28468 archaeoglob	610	1.2	130	10	Q9RXC0	Q9RXC0 arabidopsis
538	6	1.2	103	4	O8WXV1	O8WXV1 homo sapien	611	1.2	130	12	Q9IFC6	Q9IFC6 chilo iride
539	6	1.2	104	2	P95751	P95751 streptococc	612	1.2	131	13	Q98UD3	Q98UD3 xenopus lae
540	6	1.2	104	3	Q12111	Q12111 saccharomyc	613	1.2	131	17	O58137	O58137 pyrococcus
541	6	1.2	104	16	Q9KUX8	Q9KUX8 vibrio chol	614	1.2	132	4	Q9V3Y7	Q9V3Y7 homo sapien
542	6	1.2	105	15	Q9PXX6	Q9PXX6 bovine leuk	615	1.2	133	4	Q9ZBE1	Q9ZBE1 mycobacteri
543	6	1.2	105	16	O8YCQ2	Q8YCQ2 anabaena sp	616	1.2	133	4	Q9GDP7	Q9GDP7 homo sapien
544	6	1.2	106	5	Q9NTQ6	Q9NTQ6 trypanosoma	617	1.2	133	5	Q9VNS5	Q9VNS5 drosophila
545	6	1.2	106	16	Q92R68	Q92R68 rhizobium m	618	1.2	133	11	Q9D2Q4	Q9D2Q4 mus musculu
546	6	1.2	107	12	O8V559	O8V559 monkeypox v	619	1.2	134	6	Q9BDB9	Q9BDB9 tragulus ja
547	6	1.2	108	12	O41278	O41278 strawberry	620	1.2	134	10	Q9C8P3	Q9C8P3 arabidopsis
548	6	1.2	109	11	Q9JJ47	Q9JJ47 mus musculu	621	1.2	134	12	Q918P5	Q918P5 chilli leaf
549	6	1.2	109	16	O86551	O86551 streptomyce	622	1.2	134	12	Q9YVA9	Q9YVA9 gallid herp
550	6	1.2	110	9	Q38474	Q38474 bacterioph	623	1.2	134	16	Q9PFC9	Q9PFC9 xylella fas
551	6	1.2	110	16	Q9KS03	Q9KS03 vibrio chol	624	1.2	134	17	Q96Z34	Q96Z34 sulfolobus
552	6	1.2	110	17	O27031	O27031 methanobact	625	1.2	134	17	Q8U2N1	Q8U2N1 pyrococcus
553	6	1.2	110	17	Q9YDV9	Q9YDV9 aeropyrum p	626	1.2	135	6	Q9TS23	Q9TS23 bos taurus
554	6	1.2	111	12	Q91CJ7	Q91CJ7 human adeno	627	1.2	135	16	Q9X828	Q9X828 streptomyce
555	6	1.2	111	16	O8X4J8	O8X4J8 escherichia	628	1.2	135	17	Q9V091	Q9V091 pyrococcus
556	6	1.2	112	4	Q9UGV4	Q9UGV4 homo sapien	629	1.2	136	5	O97374	O97374 lymanea sta
557	6	1.2	112	13	Q98TN3	Q98TN3 platichthys	630	1.2	136	11	Q9D355	Q9D355 mus musculu
558	6	1.2	113	15	Q9WNX3	Q9WNX3 human immun	631	1.2	137	2	Q9AE00	Q9AE00 agrobacteri
559	6	1.2	113	16	Q98LD5	Q98LD5 rhizobium 1	632	1.2	137	2	Q939E0	Q939E0 pseudomonas
560	6	1.2	114	10	O8VWS7	O8VWS7 narcissus p	633	1.2	137	5	O96335	O96335 bugia mala
561	6	1.2	114	12	O8QVM2	O8QVM2 hepatitis e	634	1.2	137	10	Q9FL86	Q9FL86 arabidopsis
562	6	1.2	115	8	Q955U5	Q955U5 cheirogaleu	635	1.2	137	13	Q9PVP4	Q9PVP4 agkistrodon
563	6	1.2	115	8	Q955U0	Q955U0 cheirogaleu	636	1.2	138	12	O81447	O81447 hepatitis c
564	6	1.2	115	8	Q94PV1	Q94PV1 cheirogaleu	637	1.2	138	16	Q9HUC2	Q9HUC2 pseudomonas
565	6	1.2	115	8	Q94N60	Q94N60 cheirogaleu	638	1.2	139	6	Q29578	Q29578 sus scrofa
566	6	1.2	115	10	Q9ZRN5	Q9ZRN5 glycyrrhiza	639	1.2	139	10	Q9C7Q5	Q9C7Q5 arabidopsis
567	6	1.2	115	16	Q9AB18	Q9AB18 caulobacter	640	1.2	139	13	Q9PVE9	Q9PVE9 agkistrodon
568	6	1.2	116	10	Q94JE6	Q94JE6 oryza sativ	641	1.2	139	16	Q9KGF3	Q9KGF3 bacillus ha
569	6	1.2	116	10	O8W346	O8W346 oryza sativ	642	1.2	140	8	O79662	O79662 scomber jap
570	6	1.2	116	16	O8X2D7	O8X2D7 escherichia	643	1.2	140	8	O79664	O79664 scomber aus
571	6	1.2	117	5	Q9VZL6	Q9VZL6 drosophila	644	1.2	140	8	Q9TF613	Q9TF613 scomber jap
572	6	1.2	118	10	Q9SMW1	Q9SMW1 brassica na	645	1.2	140	10	O65171	O65171 mesembryant
573	6	1.2	119	5	O8SVR2	Q8SVR2 encephalito	646	1.2	141	10	O651D8	O651D8 oryza sativ
574	6	1.2	119	16	Q9JTR7	Q9JTR7 neisseria m	647	1.2	141	17	Q9YB15	Q9YB15 aeropyrum p
575	6	1.2	120	5	O8SXW8	O8SXW8 drosophila	648	1.2	141	17	Q9HKP1	Q9HKP1 thermoplasm
576	6	1.2	120	12	O89359	O89359 paramecium	649	1.2	142	2	Q93SJ6	Q93SJ6 myxococcus
577	6	1.2	120	15	O907P2	Q907P2 human immun	650	1.2	142	6	Q9BEC3	Q9BEC3 tragulus ja
578	6	1.2	121	4	O9BWP5	Q9BWP5 homo sapien	651	1.2	142	10	O94D16	Q94D16 oryza sativ
579	6	1.2	121	5	Q9UIA3	Q9UIA3 leishmania	652	1.2	142	12	O91RJ7	Q91RJ7 turkey herp
580	6	1.2	121	5	O8SVT6	Q8SVT6 encephalito	653	1.2	142	16	O8XZH3	O8XZH3 ralstonia s
581	6	1.2	121	16	Q9A3I4	Q9A3I4 caulobacter	654	1.2	143	5	O9GV87	O9GV87 lucina pect
582	6	1.2	124	16	P74350	P74350 synechocyst	655	1.2	143	5	O9XVB3	Q9XVB3 caenorhabdi
583	6	1.2	124	16	Q99WS4	Q99WS4 staphylococ	656	1.2	143	13	Q98TL2	Q98TL2 platichthys
584	6	1.2	124	17	O28114	O28114 archaeoglob	657	1.2	144	2	Q93DY3	Q93DY3 magnetospir
585	6	1.2	124	17	Q9HQT3	Q9HQT3 halobacteri	658	1.2	144	6	Q9BH14	Q9BH14 antilocapra
586	6	1.2	125	8	Q9TG12	Q9TG12 scomber aus	659	1.2	144	9	Q94MY8	Q94MY8 haemophilus
587	6	1.2	125	10	Q9LNU5	Q9LNU5 arabidopsis	660	1.2	144	10	Q9MAB2	Q9MAB2 arabidopsis
588	6	1.2	125	16	O8XXH6	O8XXH6 ralstonia s	661	1.2	144	16	Q91738	Q91738 pseudomonas
589	6	1.2	126	1	P95985	P95985 sulfolobus	662	1.2	144	16	O8Y1P1	O8Y1P1 ralstonia s
590	6	1.2	126	4	O96B14	Q96B14 homo sapien	663	1.2	144	17	Q9HHY6	Q9HHY6 halobacteri
591	6	1.2	126	5	O16588	O16588 caenorhabdi	664	1.2	145	2	Q9AEW4	Q9AEW4 pseudomonas
592	6	1.2	126	10	O80800	O80800 arabidopsis	665	1.2	145	2	O38724	Q38724 allium ursi
593	6	1.2	126	16	Q9A9C3	Q9A9C3 caulobacter	666	1.2	145	10	Q9SJO8	Q9SJO8 arabidopsis
594	6	1.2	126	16	Q9RKC9	Q9RKC9 streptomyce	667	1.2	145	13	Q90YX3	Q90YX3 spheeroides
595	6	1.2	127	5	Q90688	Q90688 culex pipie	668	1.2	146	5	O76915	O76915 drosophila
596	6	1.2	127	5	Q90684	Q90684 culex pipie	669	1.2	146	5	O9VG68	Q9VG68 drosophila
597	6	1.2	127	5	O90675	Q90675 culex pipie	670	1.2	147	8	Q9T9H7	Q9T9H7 halocynthia
598	6	1.2	127	8	Q9TE611	Q9TE611 scomber aus	671	1.2	147	10	O8S0H7	O8S0H7 oryza sativ
599	6	1.2	127	11	Q9DAK7	Q9DAK7 mus musculu	672	1.2	147	11	O8VD87	O8VD87 rattus ratt
600	6	1.2	127	16	Q9KNK3	Q9KNK3 vibrio chol	673	1.2	147	16	Q9CEM1	Q9CEM1 lactococcus

674	6	1.2	147	16	Q9CHX4	Q9chx4 lactococcus	747	6	1.2	158	2	Q50812	Q50812 mycobacteri
675	6	1.2	148	4	Q9UFX2	Q9ufx2 homo sapien	748	6	1.2	158	6	Q95ME6	Q95me6 sus scrofa
676	6	1.2	148	4	Q96K46	Q96k46 homo sapien	749	6	1.2	158	10	Q43759	Q43759 glycine max
677	6	1.2	148	10	Q9XHP1	Q9xhp1 sesamum ind	750	6	1.2	158	10	Q9FMH9	Q9fmh9 arabidopsis
678	6	1.2	148	10	Q8S608	Q8s608 oryza sativ	751	6	1.2	158	10	Q9SUN5	Q9sun5 arabidopsis
679	6	1.2	148	17	Q9FRK5	Q9frk5 aeropyrum p	752	6	1.2	158	10	Q8SIU3	Q8slu3 oryza sativ
680	6	1.2	149	2	Q59588	Q59588 mycobacteri	753	6	1.2	158	16	Q970A4	Q970a4 streptococ
681	6	1.2	149	11	Q8VD95	Q8vd95 beryllmys bo	754	6	1.2	158	16	Q69527	Q69527 mycobacteri
682	6	1.2	149	11	Q8VD91	Q8vd91 rattus exul	755	6	1.2	158	16	Q8X282	Q8x282 ralstonia s
683	6	1.2	149	11	Q8VD91	Q8vd91 rattus fusc	756	6	1.2	158	17	Q26301	Q26301 methanobact
684	6	1.2	149	11	Q8VD83	Q8vd83 sundanmys mu	757	6	1.2	159	4	Q9HOM9	Q9hom9 homo sapien
685	6	1.2	149	12	Q9LHN3	Q9lhn3 human polio	758	6	1.2	159	10	Q9S2Y5	Q9sz5 arabidopsis
686	6	1.2	149	12	Q9LHN3	Q9lhn3 human polio	759	6	1.2	159	16	Q9A1Q6	Q9a1q6 streptococ
687	6	1.2	149	12	Q9IHN0	Q9ihn0 human polio	760	6	1.2	160	8	Q47209	Q47209 caryota mit
688	6	1.2	149	12	Q9IHM9	Q9ihm9 human polio	761	6	1.2	160	8	Q32197	Q32197 eichhornia
689	6	1.2	149	12	Q9IHL8	Q9ihl8 human polio	762	6	1.2	160	8	Q95AX7	Q95ax7 canna sp. g
690	6	1.2	149	12	Q9IHL0	Q9ihl0 human polio	763	6	1.2	160	12	Q65859	Q65859 beet yellow
691	6	1.2	149	16	Q8XC10	Q8xc10 escherichia	764	6	1.2	160	16	Q9KSD5	Q9ksd5 vibrio chol
692	6	1.2	149	17	Q9YDS5	Q9yds5 aeropyrum p	765	6	1.2	160	16	Q99VY8	Q99vy8 staphylococ
693	6	1.2	149	17	Q8ZWS1	Q8zws1 pyrobaculum	766	6	1.2	160	16	Q8RI73	Q8ri73 fusbacteri
694	6	1.2	150	1	Q9C4Q6	Q9c4q6 methanococ	767	6	1.2	161	2	Q9S412	Q9s412 actinobacil
695	6	1.2	150	2	Q9ZGK5	Q9zgz5 leptospira	768	6	1.2	161	10	Q9SC01	Q9sc01 tremia virga
696	6	1.2	150	5	Q9V3L7	Q9v3l7 drosophila	769	6	1.2	161	10	Q8RI98	Q8ri98 nicotiana t
697	6	1.2	150	8	Q33578	Q33578 trypanosoma	770	6	1.2	161	10	Q8RI98	Q8ri98 neisseria m
698	6	1.2	150	11	Q8VD94	Q8vd94 beryllmys bo	771	6	1.2	161	16	Q9KJH8	Q9kjv8 neisseria m
699	6	1.2	150	11	Q8VD92	Q8vd92 rattus exul	772	6	1.2	161	16	Q9JY98	Q9jy98 fusbacteri
700	6	1.2	150	11	Q8VD88	Q8vd88 rattus norv	773	6	1.2	161	16	Q9AM02	Q9am02 synecococ
701	6	1.2	150	11	Q8VD86	Q8vd86 rattus ratt	774	6	1.2	162	2	Q93RE5	Q93re5 vibrio chol
702	6	1.2	150	11	Q8VD85	Q8vd85 rattus tiom	775	6	1.2	162	2	Q9N119	Q9n119 callithrix
703	6	1.2	151	4	Q9UQC1	Q9uqc1 homo sapien	776	6	1.2	162	8	Q47176	Q47176 narcissus a
704	6	1.2	151	8	Q9GOK1	Q9gok1 lampslis t	777	6	1.2	162	8	Q47177	Q47177 narcissus c
705	6	1.2	151	8	Q95AX4	Q95ax4 dioscorea b	778	6	1.2	162	8	Q47178	Q47178 narcissus r
706	6	1.2	151	16	Q9C107	Q9c107 lactococcus	779	6	1.2	162	8	Q47179	Q47179 narcissus r
707	6	1.2	151	16	Q8Z039	Q8z039 anabaena sp	780	6	1.2	162	8	Q47180	Q47180 narcissus s
708	6	1.2	151	16	Q8UGZ6	Q8ugz6 agrobacteri	781	6	1.2	162	8	Q47181	Q47181 narcissus b
709	6	1.2	152	6	Q8SQ10	Q8sq10 macaca neme	782	6	1.2	162	8	Q47182	Q47182 narcissus c
710	6	1.2	152	6	Q8SQ09	Q8sq09 papio hamad	783	6	1.2	162	8	Q47183	Q47183 narcissus h
711	6	1.2	152	6	Q8SPN5	Q8spn5 macaca mula	784	6	1.2	162	8	Q47184	Q47184 narcissus t
712	6	1.2	152	6	Q8SPF2	Q8spf2 cercopithe	785	6	1.2	162	8	Q47185	Q47185 narcissus t
713	6	1.2	152	11	Q9D416	Q9d416 mus musculu	786	6	1.2	162	8	Q47186	Q47186 narcissus t
714	6	1.2	152	11	Q8VD90	Q8vd90 rattus fusc	787	6	1.2	162	8	Q47187	Q47187 narcissus a
715	6	1.2	152	11	Q8VD89	Q8vd89 rattus norv	788	6	1.2	162	8	Q47188	Q47188 narcissus f
716	6	1.2	152	11	Q8VD84	Q8vd84 rattus tiom	789	6	1.2	162	8	Q47189	Q47189 narcissus g
717	6	1.2	153	4	Q16869	Q16869 homo sapien	790	6	1.2	162	8	Q47190	Q47190 narcissus j
718	6	1.2	153	8	Q94RE5	Q94re5 lithobius f	791	6	1.2	162	8	Q47191	Q47191 narcissus v
719	6	1.2	153	10	Q9AUD1	Q9aud1 sesamum ind	792	6	1.2	162	8	Q47192	Q47192 narcissus b
720	6	1.2	153	11	Q923T8	Q923t8 rattus norv	793	6	1.2	162	8	Q47193	Q47193 narcissus a
721	6	1.2	153	16	P77184	P77184 escherichia	794	6	1.2	162	8	Q47194	Q47194 narcissus h
722	6	1.2	154	12	Q916G3	Q916g3 hepatitis c	795	6	1.2	162	8	Q47195	Q47195 narcissus i
723	6	1.2	154	12	Q916G2	Q916g2 hepatitis c	796	6	1.2	162	8	Q47196	Q47196 narcissus p
724	6	1.2	154	12	Q916G0	Q916g0 hepatitis c	797	6	1.2	162	8	Q47197	Q47197 narcissus p
725	6	1.2	154	12	Q916F9	Q916f9 hepatitis c	798	6	1.2	162	8	Q47198	Q47198 narcissus r
726	6	1.2	154	12	Q8QQD6	Q8qqd6 hepatitis c	799	6	1.2	162	8	Q47199	Q47199 narcissus d
727	6	1.2	154	12	Q8QQD5	Q8qqd5 hepatitis c	800	6	1.2	162	8	Q47200	Q47200 narcissus e
728	6	1.2	154	12	Q8QQD4	Q8qqd4 hepatitis c	801	6	1.2	162	8	Q47201	Q47201 narcissus p
729	6	1.2	154	12	Q8QQD3	Q8qqd3 hepatitis c	802	6	1.2	162	8	Q47202	Q47202 narcissus t
730	6	1.2	154	12	Q8QQD2	Q8qqd2 hepatitis c	803	6	1.2	162	8	Q47203	Q47203 narcissus t
731	6	1.2	154	16	Q9PCE7	Q9pce7 xyella fas	804	6	1.2	162	8	Q47205	Q47205 leucojum ae
732	6	1.2	155	2	Q9L3Y9	Q9l3y9 staphylococ	805	6	1.2	162	8	Q47207	Q47207 ananas como
733	6	1.2	155	6	Q8SQ08	Q8sq08 saimiri sci	806	6	1.2	162	8	Q47208	Q47208 anigoantho
734	6	1.2	156	6	Q8SQ07	Q8sq07 saquinus oe	807	6	1.2	162	8	Q32176	Q32176 eichhornia
735	6	1.2	156	6	Q8SQ06	Q8sq06 ateles geof	808	6	1.2	162	8	Q32201	Q32201 eichhornia
736	6	1.2	156	6	Q8SQ05	Q8sq05 lagotrix l	809	6	1.2	162	8	Q32210	Q32210 eichhornia
737	6	1.2	156	6	Q8SQ04	Q8sq04 jamesbritte	810	6	1.2	162	8	Q32390	Q32390 heteranther
738	6	1.2	156	8	Q8WH47	Q8wh47 oryza sativ	811	6	1.2	162	8	Q32400	Q32400 hydrothrix
739	6	1.2	156	10	Q9LW73	Q9lw73 fuqu rubrip	812	6	1.2	162	8	Q32402	Q32402 eichhornia
740	6	1.2	156	16	Q8Z1P4	Q8z1p4 salmonella	813	6	1.2	162	8	Q32424	Q32424 heteranther
741	6	1.2	156	17	Q9YC18	Q9yc18 aeropyrum p	814	6	1.2	162	8	Q32430	Q32430 heteranther
742	6	1.2	157	2	Q8VMX2	Q8vmx2 listeria mo	815	6	1.2	162	8	Q32441	Q32441 heteranther
743	6	1.2	157	4	Q15614	Q15614 homo sapien	816	6	1.2	162	8	Q32556	Q32556 monochoria
744	6	1.2	157	5	Q9N2X7	Q9n2x7 caenorhabdi	817	6	1.2	162	8	Q32579	Q32579 monochoria
745	6	1.2	157	16	Q8Z351	Q8z351 salmonella	818	6	1.2	162	8	Q32588	Q32588 monochoria
746	6	1.2	157	17	Q8ZWR7	Q8zwr7 pyrobaculum	819	6	1.2	162	8	Q32648	Q32648 monochoria

820	1.2	162	8	Q32846	Q32846 phylodrum l	893	1.2	182	16	Q9XA05	Q9XA05 streptomyc
821	1.2	162	8	Q48289	Q48289 narcissus s	894	1.2	183	5	Q9VJ96	Q9VJ96 drosophila
822	1.2	162	8	Q48291	Q48291 narcissus b	895	1.2	183	13	Q90492	Q90492 distichodus
823	1.2	162	8	Q48365	Q48365 narcissus c	896	1.2	183	16	Q926K4	Q926K4 listeria in
824	1.2	162	16	P73165	P73165 synechocyst	897	1.2	183	16	Q8XTM6	Q8XTM6 ralstonia s
825	1.2	162	17	Q82XT7	Q82XT7 pyrobaculum	898	1.2	183	16	Q8XQAL	Q8XQAL ralstonia s
826	1.2	162	17	Q8TQT6	Q8TQT6 methanosarc	899	1.2	184	2	Q9KJL3	Q9KJL3 lactococcus
827	1.2	163	5	Q9AMK6	Q9AMK6 brugia mala	900	1.2	184	16	Q9A4F8	Q9A4F8 caulobacter
828	1.2	163	6	Q9BDC2	Q9BDC2 antilocapra	901	1.2	184	17	Q8ZKX5	Q8ZKX5 pyrobaculum
829	1.2	163	16	Q986D1	Q986D1 rhizobium l	902	1.2	185	5	Q96380	Q96380 echinococcu
830	1.2	163	16	Q9RV22	Q9RV22 deinococcus	903	1.2	185	5	Q25329	Q25329 leishmania
831	1.2	164	2	Q30747	Q30747 rhodobacter	904	1.2	185	5	Q90977	Q90977 caenorhabdi
832	1.2	164	2	Q8RTR0	Q8RTR0 pseudomonas	905	1.2	185	5	Q97161	Q97161 schistosoma
833	1.2	164	8	Q95AX2	Q95AX2 hangana ma	906	1.2	185	5	Q9W3S3	Q9W3S3 drosophila
834	1.2	164	17	Q8TLC5	Q8TLC5 methanosarc	907	1.2	185	10	Q9SVQ7	Q9SVQ7 arabidopsis
835	1.2	165	10	Q9SIT8	Q9SIT8 arabidopsis	908	1.2	186	12	Q9IX11	Q9IX11 heparitis c
836	1.2	165	10	Q98196	Q98196 nicotiana t	909	1.2	186	17	Q9YFK4	Q9YFK4 aerypyrum p
837	1.2	165	10	Q9C775	Q9C775 arabidopsis	910	1.2	187	4	Q92531	Q92531 homo sapien
838	1.2	165	10	Q8S3Y9	Q8S3Y9 sorghum bic	911	1.2	187	10	Q94D45	Q94D45 oryza sativ
839	1.2	166	2	Q93M08	Q93M08 streptomyc	912	1.2	187	17	Q8T283	Q8T283 methanopyru
840	1.2	166	4	Q96CV7	Q96CV7 homo sapien	913	1.2	188	10	Q9FMV6	Q9FMV6 arabidopsis
841	1.2	166	10	Q9LR09	Q9LR09 arabidopsis	914	1.2	188	2	Q9K429	Q9K429 mycoplasma
842	1.2	166	17	Q9YBY4	Q9YBY4 aerypyrum p	915	1.2	189	17	Q27361	Q27361 methanobact
843	1.2	167	16	Q9T325	Q9T325 pseudomonas	916	1.2	189	17	Q29411	Q29411 archaeoglob
844	1.2	167	17	Q58561	Q58561 methanococc	917	1.2	190	2	Q9ANC2	Q9ANC2 bradyrhizob
845	1.2	168	2	Q30528	Q30528 pseudomonas	918	1.2	190	5	Q9UB4	Q9UB4 mytilus edu
846	1.2	168	16	Q922E0	Q922E0 rhizobium m	919	1.2	190	10	Q942Y4	Q942Y4 oryza sativ
847	1.2	168	16	Q83512	Q83512 treponema p	920	1.2	190	12	Q99FV8	Q99FV8 human echov
848	1.2	168	16	Q8VIX9	Q8VIX9 ralstonia s	921	1.2	190	16	Q9KF21	Q9KF21 bacillus ha
849	1.2	169	4	Q9H5D8	Q9H5D8 homo sapien	922	1.2	191	2	Q86058	Q86058 azospirillu
850	1.2	169	5	Q9S508	Q9S508 drosophila	923	1.2	191	16	Q9AC38	Q9AC38 caulobacter
851	1.2	169	11	Q9D0P9	Q9D0P9 mus musculu	924	1.2	191	16	Q92NR0	Q92NR0 rhizobium m
852	1.2	169	16	Q82MT7	Q82MT7 salmonella	925	1.2	192	3	Q74887	Q74887 schizosacch
853	1.2	169	16	Q9KZA3	Q9KZA3 streptomyc	926	1.2	192	5	Q9XYV6	Q9XYV6 leishmania
854	1.2	170	5	Q8T1H6	Q8T1H6 dictyosteli	927	1.2	192	5	Q9VQ17	Q9VQ17 drosophila
855	1.2	170	8	Q9BEC1	Q9BEC1 tragus ja	928	1.2	192	10	Q9FJZ8	Q9FJZ8 arabidopsis
856	1.2	170	8	Q953M7	Q953M7 echinococcu	929	1.2	192	17	Q58289	Q58289 pyrococcus
857	1.2	170	10	Q9M0Q6	Q9M0Q6 arabidopsis	930	1.2	193	5	Q8T6C4	Q8T6C4 echinococcu
858	1.2	170	11	Q8R3S7	Q8R3S7 mus musculu	931	1.2	193	16	Q92C21	Q92C21 listeria in
859	1.2	172	6	Q9BD20	Q9BD20 macaca mula	932	1.2	193	16	Q8Y879	Q8Y879 listeria mo
860	1.2	172	12	P89250	P89250 western equ	933	1.2	194	2	Q9K428	Q9K428 mycoplasma
861	1.2	172	16	Q9RT56	Q9RT56 deinococcus	934	1.2	194	10	Q9FNG5	Q9FNG5 arabidopsis
862	1.2	172	17	Q30098	Q30098 archaeoglob	935	1.2	194	10	Q9SD84	Q9SD84 arabidopsis
863	1.2	173	16	Q9RJ35	Q9RJ35 streptomyc	936	1.2	195	10	Q9LW68	Q9LW68 arabidopsis
864	1.2	174	8	Q9ME78	Q9ME78 drosophila	937	1.2	196	2	Q9X620	Q9X620 salmonella
865	1.2	174	8	Q9MD81	Q9MD81 drosophila	938	1.2	196	10	Q82605	Q82605 arabidopsis
866	1.2	174	8	Q9MG55	Q9MG55 drosophila	939	1.2	196	12	Q56371	Q56371 grapevine l
867	1.2	175	10	Q9S718	Q9S718 arabidopsis	940	1.2	196	16	Q8ZJR2	Q8ZJR2 versinia pe
868	1.2	175	11	Q8R4W8	Q8R4W8 mus musculu	941	1.2	196	17	Q97YV7	Q97YV7 sulfolobus
869	1.2	175	12	Q9YS39	Q9YS39 lactate deh	942	1.2	197	8	Q9T5T1	Q9T5T1 potamilus i
870	1.2	175	12	Q96500	Q96500 lactate deh	943	1.2	197	8	Q8WCR6	Q8WCR6 lampsis a
871	1.2	175	13	Q91140	Q91140 nannobrycon	944	1.2	197	8	Q8WCR5	Q8WCR5 lampsis a
872	1.2	175	16	Q981I9	Q981I9 rhizobium l	945	1.2	197	8	Q8WCQ5	Q8WCQ5 villosa vil
873	1.2	176	10	Q8S524	Q8S524 oryza sativ	946	1.2	197	8	Q8WCQ4	Q8WCQ4 ligumia rec
874	1.2	176	10	Q8S2E2	Q8S2E2 oryza sativ	947	1.2	197	8	Q8WCQ1	Q8WCQ1 lampsis t
875	1.2	176	16	Q9JRC8	Q9JRC8 neisseria m	948	1.2	197	12	Q56372	Q56372 grapevine l
876	1.2	176	16	Q9JRC8	Q9JRC8 neisseria m	949	1.2	197	13	Q98TR5	Q98TR5 fugu rubrip
877	1.2	177	2	Q9FT08	Q9FT08 deinococcus	950	1.2	197	16	Q99YA7	Q99YA7 streptococc
878	1.2	177	5	Q20598	Q20598 carboxydoth	951	1.2	197	17	Q9YCA9	Q9YCA9 aerypyrum p
879	1.2	177	16	Q98PG9	Q98PG9 mycoplasma	952	1.2	198	2	Q9K4V7	Q9K4V7 mycoplasma
880	1.2	178	16	Q84475	Q84475 chlamydia t	953	1.2	198	3	Q02754	Q02754 saccharomyc
881	1.2	178	16	Q9A2V3	Q9A2V3 caulobacter	954	1.2	198	5	Q8SX04	Q8SX04 drosophila
882	1.2	178	17	Q978Q0	Q978Q0 thermoplas	955	1.2	198	11	Q61861	Q61861 mus musculu
883	1.2	179	5	Q9VX88	Q9VX88 drosophila	956	1.2	198	16	Q9RSV1	Q9RSV1 deinococcus
884	1.2	179	5	Q9VDH9	Q9VDH9 caenorhabdi	957	1.2	198	16	Q9EWR0	Q9EWR0 streptomyc
885	1.2	180	5	Q9NE73	Q9NE73 leishmania	958	1.2	199	2	Q68985	Q68985 chlorobium
886	1.2	180	10	Q9LRQ6	Q9LRQ6 arabidopsis	959	1.2	199	5	Q16026	Q16026 dirofilaria
887	1.2	180	16	Q92C81	Q92C81 listeria in	960	1.2	199	5	Q9Y082	Q9Y082 globodera r
888	1.2	180	17	Q8T7D3	Q8T7D3 methanosarc	961	1.2	199	6	Q9BG14	Q9BG14 bos taurus
889	1.2	181	10	Q49177	Q49177 oryza sativ	962	1.2	199	8	Q99503	Q99503 potamilus i
890	1.2	182	10	Q8S526	Q8S526 oryza sativ	963	1.2	199	8	Q99505	Q99505 potamilus p
891	1.2	182	10	Q8S655	Q8S655 oryza sativ	964	1.2	199	8	Q99506	Q99506 potamilus a
892	1.2	182	16	Q9HTN6	Q9HTN6 pseudomonas	965	1.2	199	8	Q99507	Q99507 potamilus c

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966 6 1.2 199 8 099508 099508 potamilus o
967 6 1.2 199 8 099509 099509 potamilus a
968 6 1.2 199 8 099510 099510 potamilus a
969 6 1.2 199 8 099511 099511 leptoidea fr
970 6 1.2 199 8 099514 099514 leptoidea c
971 6 1.2 199 8 099514 099514 leptoidea c
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ALIGNMENTS

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RESULT 1
ID Q9HCT9 PRELIMINARY; PRT; 500 AA.
AC Q9HCT9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Tumor endothelial marker 7 precursor (Tumor endothelial marker 3
DE precursor).
GN TEM7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20407466; PubMed=10947988;
RA St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.,
RA Montgomery E., Lal A., Riggins G.G., Lengauer C., Vogelstein B.,
RA Kinzler K.W.;
RT "Genes expressed in human tumor endothelium.";
RL Science 289:1197-1202(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX St Croix B., Vogelstein B., Kinzler K.W.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans.";

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Cancer Res. 61:6649-6655(2001).
DR EMBL; AF279144; AAG00869.2; -
DR EMBL; AF378753; AAL11990.1; -
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR003975; Shal_channel.
DR Pfam; PF01437; PSI; 1.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00539; NIDO; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 500 AA; 55760 MW; C545A16619EEDBED CRC64;

Query Match 100.0%; Score 500; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTVRGWNRRARESPGHVSEPD 60
Db 1 MRGELWLLVLRREARALSPQAGHDEGPGSGWAAGTVRGWNRRARESPGHVSEPD 60
QY 61 TOLSDGLGGTILAMDTLPDNRTRVVEDNHSYVVSFLYGPSEPHSRELWVDVAEANRQVK 120
Db 61 TOLSDGLGGTILAMDTLPDNRTRVVEDNHSYVVSFLYGPSEPHSRELWVDVAEANRQVK 120
QY 121 IHTILSNTHRAQSRVLSFDFPFYGHPLRQITATGGFIEMGDVTHRLMTATQVAPLMA 180
Db 121 IHTILSNTHRAQSRVLSFDFPFYGHPLRQITATGGFIEMGDVTHRLMTATQVAPLMA 180
QY 181 NFNPQYSDNSIVVFDNGTTFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
Db 181 NFNPQYSDNSIVVFDNGTTFVQWDHVLQGWEDKGSFTFOAALHHDGRIVFAYKEIPM 240
QY 241 SVPETSSQHPVKTKGLSDAFMLNPSPDVPESRRRSIFEXHRIELDPKVTSMASVEFTP 300
Db 241 SVPETSSQHPVKTKGLSDAFMLNPSPDVPESRRRSIFEXHRIELDPKVTSMASVEFTP 300
QY 301 LPTCLQHRSCDACSSDLTFNCSMCHVLQRCSSGDFRYRQEMDYGCAQEAEGRMCDQ 360
Db 301 LPTCLQHRSCDACSSDLTFNCSMCHVLQRCSSGDFRYRQEMDYGCAQEAEGRMCDQ 360
QY 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTDEDTKLNYPYAGGDLQNNLSPKTKGT 420
Db 361 DEDHDSASPDTSFSPYDGLTSSSLFIDSLTDEDTKLNYPYAGGDLQNNLSPKTKGT 420
QY 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPAMKFRSHPDHST 480
QY 481 YAEVPSGHEKEGFMABQC 500
Db 481 YAEVPSGHEKEGFMABQC 500

RESULT 2
Q9CWV5 PRELIMINARY; PRT; 500 AA.
ID Q9CWV5;
AC Q9CWV5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE 2410003107RIK protein.
GN 2410003107RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito K.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King K., Kuchiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK010361; BAB26881.1; -;
DR MGD; MGI:1919574; 2410003107Rik.
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 500 AA; 55635 MW; 802D6865F8CA18BD CRC64;

Query Match 7.0%; Score 35; DB 11; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 HQASRVLSFDFFPYGHPQLRQITATGCFIFMGD 163
DB 130 HQASRVLSFDFFPYGHPQLRQITATGCFIFMGD 164

RESULT 3
Q912V7 PRELIMINARY; PRT; 500 AA.
ID Q912V7
AC Q912V7
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Tumor endothelial marker 7 precursor.
GN 2410003107Rik OR TM7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378760; AAL1997.1; -;
DR MGD; MGI:1919574; 2410003107Rik.
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 500 TUMOR ENDOTHELIAL MARKER 7.
SQ SEQUENCE 500 AA; 55693 MW; 14FE25512A319DAF CRC64;

Query Match 7.0%; Score 35; DB 11; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 HQASRVLSFDFFPYGHPQLRQITATGCFIFMGD 163

DB 130 HQASRVLSFDFFPYGHPQLRQITATGCFIFMGD 164
RESULT 4
Q96E59 PRELIMINARY; PRT; 480 AA.
ID Q96E59
AC Q96E59
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to RIKEN CDNA 1200007L24 gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012885; AAH12885.1; -;
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
SQ SEQUENCE 480 AA; 53912 MW; F8DB0E2631BC7816 CRC64;

Query Match 2.0%; Score 10; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFFPYGH 146
DB 112 LSFDFFPYGH 121

RESULT 5
Q96PD9 PRELIMINARY; PRT; 529 AA.
ID Q96PD9
AC Q96PD9
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Tumor endothelial marker 7-related precursor.
GN TM7R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21443268; PubMed=11559528;
RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
RA Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and
RT humans";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL; AF378757; AAL11994.1; -;
DR InterPro; IPR002165; Plexin_repeat.
DR Pfam; PF01437; PSI; 1.
KW Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 529 TUMOR ENDOTHELIAL MARKER 7-RELATED.
SQ SEQUENCE 529 AA; 59583 MW; D44A0975DF894840 CRC64;

Query Match 2.0%; Score 10; DB 4; Length 529;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFFPYGH 146
DB 161 LSFDFFPYGH 170

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RESULT 6
Q9DC11 ID Q9DC11 PRELIMINARY; PRT; 530 AA.
AC Q9DC11;
AT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 1200007L24RIK protein.
OS Mus musculus (Mouse).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK004640; BAB23431.1; -
DR MGD; MGI:1914698; 1200007L24RIK.
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR003659; plexin_ext.
DR InterPro; IPR002165; plexin_repeat.
DR Pfam; PF01437; PSI; 1.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00423; PSI; 1.
SQ SEQUENCE 530 AA; 59616 MW; FB956C020735E36D CRC64;

Query Match 2.0%; Score 10; DB 11; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
DB 161 LSFDFPFYGH 170
|||||
QY 137 LSFDFPFYGH 146
DB 161 LSFDFPFYGH 170
|||||

RESULT 7
Q91ZV6 ID Q91ZV6 PRELIMINARY; PRT; 530 AA.
AC Q91ZV6;
AT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor endothelial marker 7-related precursor.
OS Mus musculus (Mouse).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21443268; PubMed=11559528;
RX Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,

Kinzler K.W., St Croix B.;
RT "Cell surface tumor endothelial markers are conserved in mice and humans.";
RL Cancer Res. 61:6649-6655(2001).
DR EMBL: AF378761; AAL11998.1; -
DR MGD; MGI:1914698; 1200007L24RIK.
DR InterPro; IPR002165; plexin_repeat.
DR Pfam; PF01437; PSI; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 31 530 POTENTIAL.
FT CHAIN 31 530 TUMOR ENDOTHELIAL MARKER 7-RELATED.
SQ SEQUENCE 530 AA; 59625 MW; FF9315020735E36D CRC64;

Query Match 2.0%; Score 10; DB 11; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 LSFDFPFYGH 146
DB 161 LSFDFPFYGH 170
|||||
QY 137 LSFDFPFYGH 146
DB 161 LSFDFPFYGH 170
|||||

RESULT 8
P94476 ID P94476 PRELIMINARY; PRT; 655 AA.
AC P94476;
AT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
DE YEBA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 TRPC2;
RX MEDLINE=88011308; PubMed=2821284;
RA Donovan W., Zheng L.B., Sandman K., Losick R.;
RT "Genes encoding spore coat polypeptides from Bacillus subtilis.";
RL J. Mol. Biol. 196:1-10(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 TRPC2;
RA Wray L., Person A., Fisher S.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168 TRPC2;
RA Borriess R., Porwollik S., Schroeter R., Hahstedt C., Mueller C.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

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RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivoita C., Roche E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitznegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium *Bacillus*
 RT *subtilis*,"
 RL Nature 390:249-256(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U51115; AAB62310.1; -;
 DR EMBL: Z99107; CAB12454.1; -;
 DR InterPro: IPR002931; Trnsglutamase_like.
 DR Pfam: PF01841; Transglut_core; 1.
 DR SMART: SM00460; TGC; 1.
 KW Complete proteome.
 SQ SEQUENCE 655 AA; 75361 MW; 74ECF63B9E1E72CA CRC64;

Query Match 1.8%; Score 9; DB 16; Length 655;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 VLAVLLVAA 439
 DB 565 VLAVLLVAA 573

RESULT 9
 Q97019 PRELIMINARY; PRT; 208 AA.
 AC Q97019;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein SRI606.
 GN SRI606.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT *Crenarchaeon*, *Sulfolobus tokodaii* strain7,"
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AF000987; BAB66684.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 208 AA; 23192 MW; D8C1DEDFA07BD9A CRC64;

Query Match 1.6%; Score 8; DB 17; Length 208;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 LLVAAIIL 442
 DB 67 LLVAAIIL 74

RESULT 10
 Q9S2F8 PRELIMINARY; PRT; 224 AA.
 AC Q9S2F8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein SCO2923.
 GN SCO2923 OR SCE19.23C.
 DN Streptomyces coelicolor.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2),"
 RL Nature 417:141-147(2002).
 DR EMBL: AL096852; CAB51004.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 224 AA; 23496 MW; 619CCAE7C8CF7A8B CRC64;

Query Match 1.6%; Score 8; DB 16; Length 224;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 GIVLAVLL 436
 DB 132 GIVLAVLL 139

RESULT 11
 Q54303 PRELIMINARY; PRT; 317 AA.
 ID Q54303
 AC Q54303;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Methyltransferase.
 GN RAPM.
 OS Streptomyces hygroscopicus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1912;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 5491;
 RX MEDLINE=95372374; PubMed=7644502;
 RA Schwecke T., Aparicio J.F., Molnar I., Koenig A., Khaw L.E.,
 RA Haydock S.F., Orlinnyk M., Caffrey P., Cortes J., Lester J.B.,
 RA Boehm G.A., Staunton J., Leadlay P.F.;
 RT "The biosynthetic gene cluster for the polyketide immunosuppressant
 RT rapamycin,"
 RL proc. Natl. Acad. Sci. U.S.A. 92:7839-7843(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL 5491;
 RX MEDLINE=96186895; PubMed=8635730;
 RA Molnar I., Aparicio J.F., Haydock S.F., Khaw L.E., Schwecke T.,
 RA Koenig A., Staunton J., Leadlay P.F.;
 RT "Organisation of the biosynthetic gene cluster for rapamycin in

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RT Streptomyces hygroscopicus: analysis of genes flanking the polyketide
RL synthase."
RN Gene 169:1-7(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-NREL 5491;
RX MEDLINE=96186896; PubMed=8635756;
RA Aparicio J.F., Molnar I., Schwecke T., Koenig A., Haydock S.F.,
RA Khaw L.E., Staunton J., Leadlay P.F., Staunton J., Leadlay P.F.;
RT "Organization of the biosynthetic gene cluster for rapamycin in
RT Streptomyces hygroscopicus: analysis of the enzymatic domains in the
RT modular polyketide synthase."
RL Gene 169:9-16(1996).
DR EMBL; X86780; CAA60466.1; -.
DR InterPro; IPR000051; SAM_bind.
KW Transferase.
SQ SEQUENCE 317 AA; 35065 MW; 42F6A477FDAC0011 CRC64;

Query Match 1.6%; Score 8; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LREAARAL 19
DB 188 LREAARAL 195
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RESULT 12
Q9HQA6 PRELIMINARY; PRT; 363 AA.
AC Q9HQA6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Vng1250h.
GN VNG1250H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RW EMBL; AE005050; AAG19609.1; -.
KW Complete proteome.
SQ SEQUENCE 363 AA; 37543 MW; A1CD167FA482ABED CRC64;

Query Match 1.6%; Score 8; DB 17; Length 363;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 LAVLLVAA 439
DB 17 LAVLLVAA 24
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RESULT 13
Q9AC73 PRELIMINARY; PRT; 429 AA.
AC Q9AC73;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 21, Last annotation update)
KW Complete proteome.

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DE Arsenic efflux pump protein.
GN ARSB OR SAP017.
OS Staphylococcus aureus (strain N315).
OG Plasmid pN315.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003139; BAB43886.1; -.
DR InterPro; IPR000802; Ars_pump.
DR Pfam; PF02040; Arsb; 1.
DR PRINTS; PR00758; ARSENICPUMP.
DR TIGRFAMS; TIGR00935; 2a45; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 429 AA; 46469 MW; 654CFB2A1C9A0ADB CRC64;

Query Match 1.6%; Score 8; DB 16; Length 429;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 IVLAVLLV 437
DB 230 IVLAVLLV 237
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RESULT 14
Q9JYC8 PRELIMINARY; PRT; 472 AA.
AC Q9JYC8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Amino acid symporter, putative.
GN NMB1647.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
RW EMBL; AE002515; AAF41996.1; -.
TIGR; NMB1647; -.
DR InterPro; IPR002293; AA/rel_pmeasel.
DR InterPro; IPR001463; Na/Ala_symptr.
DR Pfam; PF01235; Na_Ala_symp; 1.
DR PRINTS; PR00175; NAALASMPORT.
DR TIGRFAMS; TIGR00835; agcs; 1.
DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
KW Complete proteome.

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SQ SEQUENCE 472 AA; 50465 MW; 6EAD257B41C7D68F CRC64;

Query Match 1.6%; Score 8; DB 16; Length 472;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 VGIIVLAVL 435

Db 195 VGIIVLAVL 202

RESULT 15

Q9JTB1 PRELIMINARY; PRT; 472 AA.
AC Q9JTB1; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative sodium:alanine symporter.
GN NMA1901
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; Pubmed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491."
RL Nature 404:502-506(2000).
DR EMBL; AL162757; CAB85122.1;
DR InterPro; IPR002293; AA/rel_primeasel.
DR InterPro; IPR001463; Na/Ala_symptr.
DR Pfam; PF01235; Na_Ala_symp; 1.
DR PRINTS; PR00175; NAALASMPOR.
DR TIGRFAMs; TIGR00835; agcs; 1.
DR PROSITE; PS00873; NA_ALANINE_SYMP; 1.
KW Complete proteome.
SQ SEQUENCE 472 AA; 50457 MW; 6FELD6BC5DB68694 CRC64;

Query Match 1.6%; Score 8; DB 16; Length 472;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 VGIIVLAVL 435

Db 195 VGIIVLAVL 202

Search completed: April 22, 2003, 16:18:52
Job time : 118 secs

